baci mycc haen	 H +	finds:	: 225	len	: 921/	ck:	
bacillus subtilis. mycoplasma pirum. haemophilus influe							SW:CDSN_PIG
bacillus subtilis. mycoplasma pirum.		finds:	: 288	len	: 8973	ck:	SW:CDSA_HAEIN
bacillus subtilis.	 L	finds:	: 133	len	: 6718	ck:	SW:CDD_MYCPI
man mancaras	 L	finds:	: 136	len:	: 9048	ck:	SW:CDD_BACSU
! P49070 mus musculus (mouse)	 L	finds:	: 294	len:	: 283	ck:	SW:CAMG_MOUSE
! P54657 dictyostelium discoide		finds:	: 213	len:	: 3813	Ωk:	SW:CAD1_DICDI
! P33967 bacillus cereus. blast	. 1	finds:	: 140	len:	: 8425	ck:	SW:BSR_BACCE
! P80492 branchiostoma floridae	 L	finds:	: 440	len:	: 391	ck:	SW:BRA2_BRAFL
! Q17134 branchiostoma floridae	 L	finds:	: 448	len:	: 7365	ck:	SW:BRA1_BRAFL
! Q01851 homo sapiens (human).	 1	finds:	: 423	len:	: 2610	ck:	SW:BR3A_HUMAN
! P08694 pseudomonas pseudoalca	:-	finds:	: 275	len:	: 1527	ck:	SW:BPHB_PSEPS
! P30884 xenopus laevis (africa		finds:	: 398	len:	:: 1620	ck:	SW:BMPB_XENLA
! P25703 xenopus laevis (africa		finds:	: 398	len:	:: 9714	ck:	SW:BMPA_XENLA
! P09354 bacillus ps3 (thermoph	 µ	finds:	: 127	len:	: 4392	ck:	SW:ATPZ_BACP3
! P30049 homo sapiens (human).	μ	finds:	: 168	len:	:: 1686	ck:	SW:ATPD_HUMAN
! Q35584 pongo pygmaeus (orangu	:: 1	finds:	: 68	len:	:: 3550	ck:	SW:ATP8_PONPY
! P92896 pongo pygmaeus pygmaeu	:: 1	finds:	: 68	len:	:: 3460	ck:	SW:ATP8_PONPP
! P92694 pongo pygmaeus abelii	1	finds:	: 68	len:	:: 3336	ck:	SW:ATP8_PONPA
! Q02653 podospora anserina. atp	;; µ	finds:	: 50	len:	:: 8763	ck:	SW:ATP8_PODAN
! P48201 homo sapiens (human)	;; 1	finds:	: 142	len:	: 2178	ck:	SW:AT93_HUMAN
! Pl1446 escherichia coli. n-ac	;; -	finds:	: 334	len:	t: 6342	c):	SW:ARGC_ECOLI
! Q91555 xenopus laevis (africar	, L	finds:	: 360	len:	: 4724	ck:	SW: ARG3_XENLA
! Q91554 xenopus laevis (african	;; 	finds:	: 360	len:	: 4641	ck:	SW:ARG2_XENLA
! Q91553 xenopus laevis (african	;; 1	finds:	: 360	len:	c: 4321	ck:	SW: ARG1_XENLA
! P24801 xenopus laevis (africa	;; 1	finds:	: 339	len:	t: 6452	ck:	SW:ANX2_XENLA
! Q00831 citrobacter freundii,	;; 1	finds:	187	len:	c: 4831	ck:	SW:AMPD_CITER
! P18539 serratia marcescens	:: 1	finds:	1: 376	len:	<: 107	ck:	SW:AMPC_SERMA
! P33772 salmonella typhimurium	3: 1	finds:	1: 289	len:	ck: 5663		SW: AMIA_SALTY
! Q56346 treponema pallidum.	". ⊢ .	finds:	1: 357	len:	ck: 255	-	SW:ALR_TREPA
! P09369 drosophila mojavensis	3:	finds:	1: 253	len:	ck: 8528		SW:ADH2_DROMO
! P80643 bacillus subtilis. acy	: -	finds:	1: 77	len:	ck: 8148		SW:ACP_BACSU
! Q09138 sus scrofa (pig). 5'-	š: 1	finds:	1: 133	len:	ck: 8859		SW:AAKG_PIG
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,T,S)(R,K,H	7, M, A,	,S)(L,I,V	X(P,T	, A, P)	C,I,V,M	003 (1	1 <(X){1,20
	ches	0 mismatches	allowing		SWISS-Prot:*	VISS	FINDPATTERNS On SW

523 rattus norvegicus (r	! Q64623	finds: 1	len: 367	ck: 6443 1	SW:DUS1_RAT
563 mus musculus (mouse)	! P28	finds: 1	en: 367	ck: 5871 l	SW:DUS1_MOUSE
28562 homo sapiens (human)		finds: 1	en: 367	ck: 5401 l	SW:DUS1_HUMAN
578 vibrio alginolyticus	! 056578	finds: 1	len: 165	ck: 2736 1	SW:DSBB_VIBAL
577 bacillus subtilis. d	L ! P39577	finds: 1	len: 252	ck: 2631 l	SW:DLTE_BACSU
177 streptomyces cinnamo	l ! P41177	finds: 1	en: 261	ck: 4473 l	SW:DHKR_STRCM
542 streptomyces violace	l ! P16542	finds: 1	en: 272	ck: 3104 1	SW:DHK1_STRVN
727 rattus norvegicus (r	1 ! P47727	finds: 1	en: 276	ck: 3202 1	SW:DHCA_RAT
844 oryctolagus cuniculu	1 ! P47844	finds:	en: 276	ck: 1426 1	SW:DHCA_RABIT
8758 mus musculus (mouse)	1 ! P48	finds:	en: 276	ck: 204 1	SW:DHCA_MOUSE
6152 homo sapiens carbony	1 ! P16	finds:	en: 276	ck: 3202 1	SW:DHCA_HUMAN
828 homo sapiens (human)	1 ! 075	finds:	en: 276	ck: 391 1	SW:DHC3_HUMAN
314 anas platyrhynchos (1 ! 057314	finds:	en: 312	ck: 9157 l	SW:DHBX_ANAPL
503 mus musculus (mouse)	1 ! 070503	finds:	len: 312	ck: 4788]	SW:DHBK_MOUSE
939 rattus norvegicus (r	1 ! 054939	finds:	len: 306	ck: 3366]	SW:DHB3_RAT
p70385 mus musculus (mouse)	1 ! ₽70	finds:	en: 305	ck: 9317 1	SW:DHB3_MOUSE
P37058 homo sapiens (human)	1 ! P37	finds:	en: 310	ck: 3434 l	SW:DHB3_HUMAN
477 klebsiella pneumonia	1 ! Q59477	finds:	en: 387	ck: 846	SW:DHAT_KLEPN
P45513 citrobacter freundii	1 ! P45	finds:	en: 387	ck: 101	SW:DHAT_CITER
Q54433 streptococcus mutans	1 ! 054	finds:	len: 145	ck: 9135 1	SW:DFP_STRMU
P20449 saccharomyces cerevi	1 ! P20	finds:	len: 482	ck: 2958 1	SW:DBP5_YEAST
P39042 streptomyces sp. (st	1 ! P39	finds:	len: 291	ck: 4817 1	SW:DACX_STRSK
P27111 escherichia coli. cy	1 ! P27	finds:	len: 299	ck: 4304	SW:CYNR_ECOLI
P00098 rhodocyclus tenuis (1 ! 100	finds:	len: 92	ck: 2620	SW:CY2_RHOTE
P80675 blaberus craniifer.	1 ! P80	finds:	len: 127	ck: 1926	SW:CUO4_BLACR
P12946 bacillus subtilis. c	1 ! P12	finds:	len: 306	ck: 1522	SW:CTAA_BACSU
Q04443 bacillus firmus. cyt	1 ! Q04	finds:	len: 297	ck: 716	SW:CTAA_BACFI
P40715 escherichia coli. su	1 ! P40	finds:	len: 331	ck: 8969	SW:CSCR_ECOLI
21727 pisum sativum (garde	1 ! P21	finds:	len: 402	ck: 5889	SW:CPTR_PEA
81580 cancer pagurus (rock	1 ! P81	finds:	len: 114	ck: 1605	SW:CPC1_CANPG
79010 schizosaccharomyces	1 ! P79	finds:	len: 164	ck: 7810	SW:COX4_SCHPO
P14058 schizophyllum commun	1 ! P14	finds:	len: 268	ck: 7659	SW:COX3_SCHCO
P36562 escherichia coli. ni	1 ! P36	finds:	len: 359	ck: 7029	SW:COBT_ECOLI
P03598 tobacco streak virus	1 ! PO:	finds:	len: 237	ck: 3595	SW:COAT_TOBSV
P06663 turnip crinkle virus	1 ! ₽06	finds:	len: 351	ck: 1818	SW:COAT_TCV
P40685 rhodobacter sphaeroi	1 ! P4(finds:	len: 213	ck: 8138	SW:CHRR_RHOSH

SW	i P52094 escherichia coli. histi	inds: 1	1: 228 f	7651 Ken	ck:	SW: HISO_ECOLI
	! P10369 salmonella typhimurium.	finds: 1	359	516 ¡len:	c):	SW: HIS8_SALTY
9 0	! P04233 homo sapiens (human). h	finds: 1	296	9949 len:	ck:	SW:HG2A_HUMAN
S W	! P50200 clostridium sordellii.	finds: 1	267	1047 len:	ck:	SW: HDHA_CLOSO
SE	! P04187 mus musculus (mouse). 9	finds: 1	247	92 len:	ck:	SW:GRAB_MOUSE
SW	! P35411 rattus norvegicus (rat)	finds: 1	354	4478 len:	ck:	SW:GPRD_RAT
S W	! P49238 homo sapiens (human). p	finds: 1	355	2863 len:	ck:	SW:GPRD_HUMAN
n c	! P37606 escherichia coli. glyce	finds: 1	339	4443 len:	ck:	SW:GPDA_ECOLI
o c	! Q28914 pan troglodytes (chimpa	finds: 1	123	149 len:	c) :	SW:GLPB_PANTR
W W	! O18830 ovis aries (sheep). gro	finds: 1	375	1548 len:	c) :	SW:GDF8_SHEEP
n u	! 035312 rattus norvegicus (rat)	finds: 1	376	1496 len:	ck:	SW:GDF8_RAT
e se	! O18831 sus scrofa (pig). growt	finds: 1	375	1805 len:	ck:	SW:GDF8_PIG
n u	! O18828 papio hamadryas (hamadr	finds: 1	375	1463 len:	ck:	SW:GDF8_PAPHA
CIA W	i 008689 mus musculus (mouse). g	finds: 1	376	2293 len:	с к :	SW:GDF8_MOUSE
Sig. S	i 014793 homo sapiens (human). g	finds: 1	375	1814 len:	ck:	SW:GDF8_HUMAN
33	! O18836 bos taurus (bovine). gr	finds: 1	375	9403 len:	ck:	SW:GDF8_BOVIN
e s	! P41347 zea mays (maize). ferre	finds: 1	152	4642 len:	ck:	SW:FTRC_MAIZE
e c	! P01100 homo sapiens (human). p	finds: 1	380	4677 len:	ck:	SW:FOS_HUMAN
S 32	! P11939 gallus gallus (chicken)	finds: 1	367	7007 len:	ck:	SW:FOS_CHICK
o (6	! P23050 avian retrovirus nk24.	finds: 1	322	9324 len:	ck:	SW:FOS_AVINK
0 0	! P23449 bacillus subtilis. prob	finds: 1	208	1150 len:	ck:	SW:FLIH_BACSU
	! P37925 salmonella typhimurium.	finds: 1	335	6074 len:	ck:	SW:FIMH_SALTY
S S	P28891 agkistrodon contortrix	finds: 1	203	7566 len:	ck:	SW:FIBR_AGKCO
	! P28901 shigella flexneri. ferr	finds: 1	135	1251 len:	c):	SW:FENR_SHIFL
n u	! P28861 escherichia coli. ferre	finds: 1	247	3071 len:	ck:	SW: FENR_ECOLI
Ç. (! P55336 vibrio harveyi. 3-oxoad	finds: 1	244	5984 len:	ck:	SW:FABG_VIBHA
13	! O54438 pseudomonas aeruginosa.	finds: 1	247	9922 len:	ck:	SW:FABG_PSEAE
	! P43713 haemophilus influenzae.	finds: 1	242	4159 len:	ck:	SW:FABG_HAEIN
S	! P25716 escherichia coli. 3-oxc	finds: 1	244	3492 len:	ck:	SW:FABG_ECOLI
0 4	! P95376 neisseria meningitidis.	finds: 1	144	5831 len:	ck:	SW:EXBD_NEIME
5 T	! 006434 neisseria gonorrhoeae.	finds: 1	144	4894 len:	ck:	SW:EXBD_NEIGO
n (4	: 033096 mycobacterium leprae. e	finds: 1	318	3764 len:	ck:	SW:ETFA_MYCLE
n u	! Q90257 brachydanio rerio (zebr	finds: 1	270	1627 len:	ck:	SW:ES1_BRARE
C 25	! P39704 saccharomyces cerevisia	finds: 1	215	5386 len:	ck:	SW:ERP2_YEAST
n o	! Q29143 trichosurus vulpecula (finds: 1	102	5524 len:	Ċ.	SW:ELAC_TRIVU
S S	! P08761 drosophila melanogaster	finds: 1	255	68 len:	ck:	SW:EI28_DROME
Q.	P35621 brachydanio rerio (zebr	finds: 1	355	2951 len:	ck:	SW:DVR1_BRARE

SW:NUOJ_ECOLI	SW:NUKM_BRAOL	SW:NUHM_NEUCR	SW:NU6M_APILI	SW: NU5M_ANSCE	SW:NU1M_COTJA	SW:NOR1_ASPPA	SW:NIFY_KLEPN	SW:NEUB_XENLA	SW:MTDA_METEX	SW:MML6_MYCTU	SW:MLPA_MYXXA	SW:MESJ_HAEIN	SW:MDH_RHILV	SW:MAUF_PARDE	SW:LSPA_MYCTU	SW:KR1_HSVBS	SW:KDUD_BACSU	SW: ISIA_SYNY3	SW:IS12_STRAL	SW:IPRA_SAGSA	SW: IMPB_SALTY	SW: IMMN_ECOLI	SW:IDNR_ECOLI	SW:IDI_MYCTU	SW:ICW3_PSOTE	SW:ICE2_RAT	SW:IAA5_WHEAT	SW:IAA2_WHEAT	SW:IAA1_WHEAT	SW:HYCD_ECOLI	SW:HUPK_RHILV	SW:HPRK_BACSU	SW:HMPH_MOUSE	SW:HMPH_HUMAN
ck: 2909 ck: 7750	ck: 9647	ck: 3961	ck: 6545	ck: 1655	ck: 6471	ck: 7169	ck: 8799	ck: 1414	ck: 9524	ck: 4418	ck: 8809	ck: 1410	ck: 1419	ck: 7474	ck: 2319	ck: 5295	ck: 3484	ck: 4153	ck: 4079	ck: 1378	ck: 6434	ck: 6528	ck: 2843	ck: 9024	ck: 7697	ck: 8827	ck: 4073	ck: 4825	ck: 3320	ck: 675	ck: 1548	ck: 4393	ck: 8616	ck: 3785
len: 184 len: 201	len: 215	len: 263	len: 167	len: 214	len: 72	len: 271	len: 229	len: 120	len: 288	len: 397	len: 236	len: 430	len: 320	len: 277	len: 202	len: 467	len: 254	len: 342	len: 256	len: 181	len: 424	len: 131	len: 332	len: 203	len: 207	len: 312	len: 124	len: 123	len: 124	len: 307	len: 370	len: 309	len: 271	len: 270
finds: 1 finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1
P33605 escherichia coli. na	! P42027 brassica oleracea (c	! P40915 neurospora crassa. n	! P34857 apis mellifera ligus	! Q31651 anser caerulescens (! P24968 coturnix coturnix ja.	! Q00278 aspergillus parasiti	! P09135 klebsiella pneumonia	! P43443 xenopus laevis (afri	! P55818 methylobacterium ext	! Q10773 mycobacterium tuberc	! P38371 myxococcus xanthus.	! P44689 haemophilus influenz	! 033525 rhizobium leguminosa	! P29897 paracoccus denitrifi	! Q10764 mycobacterium tuberc	! Q08097 bovine herpesvirus t	P50842 bacillus subtilis. 2	! Q55274 synechocystis sp. (s	! P23393 streptomyces albus g	! P31608 sagittaria sagittifo	! P18642 salmonella typhimuri	P09182 escherichia coli. co	! P39343 escherichia coli. 1-	! P72002 mycobacterium tuberc	! P10822 psophocarpus tetrago	! P55215 rattus norvegicus (r	! P01084 triticum aestivum (w	! P01083 triticum aestivum (w	! P01085 triticum aestivum (w	! P16430 escherichia coli. fo	! P28153 rhizobium leguminosa	: 034483 bacillus subtilis. h	! P43120 mus musculus (mouse)	! Q03014 homo sapiens (human)

: + : FO8/06 Lycopersicon esculentum	111102	:			
. 1	÷	en · 181	5240 1	<u>و</u>	SW:RBS1_LYCES
: 1 ! P10647 solanum tuberosum (r	finds	en: 181	4699 1	ck: 4	SW:RBSO_SOLTU
: 1 ! P25544	finds	len: 302	4295 1	ck: 4	SW:RBCR_CHRVI
s: 1 ! Q27297 drosophila melanogaster	finds:	len: 336	2533 1	ck:	SW:RA51_DROME
s: 1 ! P25983 bacillus subtilis. dihy	finds:	.en: 256	2658 1	ck:	SW:PYRZ_BACSU
3: 1 ! P96174 vibrio sp. (strain 2693	finds:	en: 310	5096 1	ck:	SW:PYRB_VIBS2
1 ! P19910 serratia marcescens. as	finds:	.en: 305	4826 1	ck:	SW:PYRB_SERMA
s: 1 ! P08420 salmonella typhimurium.	finds:	len: 310	2583]	ck:	SW:PYRB_SALTY
s: 1 ! 058451 pyrococcus horikoshii.	finds:	len: 308	9980]	ck:	SW:PYRB_PYRHO
s: 1 ! P77918 pyrococcus abyssi. aspa	finds:	len: 308	9304]	ck:	SW:PYRB_PYRAB
s: 1 ! P71808 mycobacterium tuberculc	finds:	len: 319	1547]	ck:	SW:PYRB_MYCTU
1 ! P00479 escherichia coli.	finds:	len: 310	3945	ck:	SW:PYRB_ECOLI
1 ! 026272 methanobacter	finds:	len: 248	5550	ck:	SW:PUR7_METTH
s: 1 ! P50452 homo sapiens (human). d	finds:	len: 374	4145	ck:	SW:PTI8_HUMAN
s: 1 ! P35237 homo sapiens (human). p	finds:	len: 376	300	ck:	SW:PTI6_HUMAN
1 ! P54530 bacillus subtilis. pr	finds:	len: 299	158	ck:	SW:PTB_BACSU
1 : P15781 bos taurus (finds:	len: 79	7861	œk:	SW:PSPB_BOVIN
s: 1	finds:	len: 331	609	ck:	SW:PME_ASPTU
s: 1 ! Q12535 aspergillus aculeatus.	finds:	len: 331	2447	ck:	SW:PME_ASPAC
s: 1 ! Q12639 mycosphaerella pinodes	finds:	len: 299	8743	ck:	SW:PLYA_MYCPO
ls: 1 ! P08567 homo sapiens (human). p) finds	len: 350	1536	ck:	SW:PLEK_HUMAN
ls: 1 ! P21697 synechocystis sp. (stra	5 finds	len: 126	6628	ö K:	SW:PLAS_SYNY3
ls: 1 ! Q40708 oryza sativa (rice). pi	3 finds:	len: 263	1305	ck:	SW:PI7A_ORYSA
ls: 1 ! P16678 escherichia coli. phosp	2 finds:	len: 252	804	ck:	SW:PHNK_ECOLI
ls: 1 ! P14697 alcaligenes eutrophus.	6 finds:	len: 246	2829	ck:	SW:PHBB_ALCEU
ds: 1 ! P28795 saccharomyces cerevisia	1 finds:	len: 441	166	ck:	SW:PEX3_YEAST
ds: 1 ! P31078 rhodobacter capsulatus	6 finds:	len: 166	1875	ck:	SW:PETP_RHOCA
ds: 1 ! Q15077 homo sapiens (human). p	8 finds:	len: 328	7545	ck:	SW:P2Y6_HUMAN
ds: 1 ! Q99489 homo sapiens (human). d	l finds:	len: 341	7167	ck:	SW:OXDD_HUMAN
1 ! P31228	1 finds:	len: 341	9943	ck:	SW:OXDD_BOVIN
1 ! P31317 schizosacch	7 finds:	len: 327	9240	ck:	SW:OTC_SCHPO
ds: 1 ! P96172 vibrio sp. (strain 2693	1 finds:	len: 301	7498	ck:	SW:OTCA_VIBS2
ds: 1 ! P28678 drosophila pseudoobscur	4 finds:	len: 374	7241	ck:	SW:OPS1_DROPS
ds: 1 ! P06002 drosophila melanogaster	3 finds:	len: 373	4358	ck:	SW:OPS1_DROME
1 ! P22269 calliphora	1 finds:	len: 371	9791	ck:	SW:OPS1_CALVI
1 ! P08005 salmonella typhimu	6 finds:	len: 306	4920	ck:	SW:OPPB_SALTY
ds: 1 ! P31132 escherichia coli. oligd	6 finds	len: 306	5147	čķ:	SW:OPPB_ECOLI

ds: 1 ! P44847 haemophilus influenz	len: 311 finds	ck: 4	SW:SUFI_HAEIN
ds: 1 ! Q41495 solanum tuberosum (p	len: 214 finds	ck: 5285	SOLTU
ds: 1 ! P43308 homo sapiens (human)	len: 183 finds	ck: 8093 l	HUMAN
ds: 1 ! P23438 canis familiaris (do	len: 183 finds	ck: 8392	SW:SSRB_CANFA
ds: 1 ! P28646 rattus norvegicus (r	len: 391 finds	ck: 9240	SW:SSR1_RAT
finds: 1 ! P30873 mus musculus (mouse)	len: 391 fin	ck: 8110	SW:SSR1_MOUSE
ds: 1 ! P30872 homo sapiens (human)	len: 391 finds	ck: 8652	SW:SSR1_HUMAN
ds: 1 ! P96069 salmonella typhimuri	len: 352 finds	ck: 3263	SW:SSAU_SALTY
finds: 1 ! P28164 chlamydia psittaci.	len: 134 fir	ck: 9648	SW:SRP_CHLPS
finds: 1 ! P21625 spiroplasma mellifer	len: 241 fir	ck: 9527	SW:SPIR_SPIME
finds: 1 ! P39444 salmonella typhimuri	len: 432 fir	ck: 7477	SW:SPAL_SALTY
finds: 1 ! P44164 haemophilus influenz	len: 164 fir	ck: 2974	SW:SIXA_HAEIN
finds: 1 ! P76502 escherichia coli. ph	len: 161 fi	ck: 9360	SW:SIXA_ECOLI
finds: 1 09zcs5 rickett sia prowazeki	len: 433 fi	ck: 3620	SW:SECY_RICPR
finds: 1 P26428 escherichia coli. si	len: 217 fi	ck: 54	SW:S27A_ECOLI
finds: 1 ! Q56214 thermus aquaticus (s	len: 324 f i	ck: 3575	SW:RUVB_THETH
inds: 1 ! P73307 synechocystis sp. (s	len: 133 fi:	ck: 8926	SW:RS8_SYNY3
inds: 1 ! P41117 acholeplasma axanthu	len: 257 fi	ck: 7310	SW:RS3_ACHAX
inds: 1 ! P28189 schizosaccharomyces	len: 150 fi	ck: 3858	SW:RS13_SCHPO
inds: 1 ! P06362 marchantia polymorph	len: 132 fi	ck: 6002	SW:RR8_MARPO
inds: l ! P24613 spinacia oleracea (s	len: 256 fi	ck: 718	SW:RK21_SPIOL
inds: 1 ! P22851 luffa cylindrica (sm	len: 250 fi	ck: 7681	SW:RIPB_LUFCY
inds: 1 ! 000465 luffa cylindrica (sm	len: 277 fi	ck: 429	SW:RIPA_LUFCY
inds: 1 ! 028272 archaeoglobus fulgid	len: 219 fi	ck: 4460	SW:RIB7_ARCFU
inds: 1 ! P52198 homo sapiens (human)	len: 227 fi	ck: 2901	SW:RHO7_HUMAN
finds: 1 ! Q28849 macaca mulatta (rhes	len: 416 fi	ck: 4371	SW:RHL_MACMU
finds: 1 ! P37761 neisseria gonorrhoea	len: 346 fi	ck: 5086	SW:RFBB_NEIGO
finds: 1 ! P03872 saccharomyces cerevi	len: 296 fi	ck: 6596	SW:REP2_YEAST
finds: 1 ! P52574 tortula ruralis (mos	len: 218 fi	ck: 4850	SW:REHY_TORRU
inds: 1 ! Q94913 drosophila melanogas	len: 298 fi	ck: 7903	SW:REG5_DROME
inds: 1 ! 024045 musa acuminata (bana	len: 180 fi	ck: 2518	SW:RBS_MUSAC
inds: 1 ! 060116 schizosaccharomyces	len: 318 fi	ck: 3214	SW:RBSK_SCHPO
inds: 1 ! P32764 solanum tuberosum (p	len: 181 f:	ck: 4433	SW:RBS3_SOLTU
finds: 1 ! P07179 lycopersicon esculen	len: 180 f :	ck: 4535	SW:RBS2_LYCES
finds: 1 ! P26574 solanum tuberosum (p	len: 181 f:	ck: 4863	SW:RBS1_SOLTU
finds: 1 ! P04714 petunia sp. (petunia	len: 180 f:	ck: 2967	SW:RBS1_PETSP

agrobacterium rhizogene	P13461	H	finds:	147	len:	2761	ck:	SW:VID1_AGRRA
agrobacterium tumefacie	1 205357	1	finds:	230	len:	2826	ck:	SW:VIB8_AGRT9
agrobacterium tumefacie	P09781	_	finds:	230	len:	2646	ck:	SW:VIB8_AGRT6
agrobacterium tumefacie	1 P17798	1	finds:	237	len:	5994	ck:	SW:VIB8_AGRT5
herpesvirus saimiri (st	901017	1	finds:	366	len:	7071	ck:	SW:VGLM_HSVSA
herpes simplex virus (t	P13291	ם	finds:	372	len:	501	ck:	SW:VGLI_HSV2H
bacteriophage g4. major	P03644	1	finds:	177	len:	4484	ck:	SW:VGG_BPG4
bacteriophage p22. eaa	! Q03544	1	finds:	317	len:	7758	ck:	SW:VEAA_BPP22
human papillomavirus ty	P36796	_	finds:	368	len:	4491	ck:	SW:VE2_HPV52
human papillomavirus ty	P26547	ר	finds:	358	len:	1816	ck:	SW:VE2_HPV51
human papillomavirus ty	P36794	ъ	finds:	368	len:	5828	ck:	SW:VE2_HPV45
human papillomavirus ty	1 P17383	μ-	finds:	372	len:	9656	ck:	SW:VE2_HPV31
human papillomavirus ty	P25482	1	finds:	391	len:	734	ck:	SW:VE2_HPV2A
human papillomavirus ty	! P50771	1	finds:	376	len:	1816	ck:	SW:VE2_HPV28
human papillomavirus ty	P06790	ב	finds:	365	len:	5006	ck:	SW:VE2_HPV18
human papillomavirus ty	P36781	μ	finds:	376	len:	273	ck:	SW:VE2_HPV10
human papillomavirus ty	! P36778	щ	finds:	383	len:	4819	ck:	SW:VE2_HPV03
enterococcus faecium (s	906240	Н	finds:	384	len:	3601	ck:	SW: VANS_ENTFC
equine herpesvirus type	P32517	Н	finds:	303	len:	5996	ck:	SW:US02_HSVEK
escherichia coli. umud	P04153	μ	finds:	139	len:	8403	ck:	SW:UMUD_ECOLI
drosophila melanogaster	P52487	Р	finds:	153	len:	1891	ck:	SW:UBC7_DROME
dendroaspis angusticeps	P01404	نر	finds:	81	len:	8703	ck:	SW:TXF8_DENAN
rattus norvegicus (rat)	P23441		finds:	372	len:	6608	ck:	SW:TTF1_RAT
mus musculus (mouse). t	P50220	ъ	finds:	372	len:	7622	ck:	SW:TTF1_MOUSE
homo sapiens (human). t	P43699	ם	finds:	371	len:	5439	ck:	SW:TTF1_HUMAN
canis familiaris (dog).	P43698	1	finds:	371	len:	4988	ck:	SW:TTF1_CANFA
cryptococcus neoformans	P27710	μ	finds:	312	len:	2342	ck:	SW:TRPF_CRYNE
datura stramonium (jims	P50165	<u> </u>	finds:	268	len:	5293	ck:	SW:TRNH_DATST
saccharomyces cerevisia	1 Q12093	1	finds:	417	len:	8415	ck:	SW:TRMU_YEAST
schizosaccharomyces pom	013947	H	finds:	415	len:	7997	ck:	SW:TRMU_SCHPO
synechocystis sp. (stra	P72828	ц	finds:	231	len:	6210	ck:	SW:TRMD_SYNY3
agrobacterium tumefacie	! Q57471	Д	finds:	102	len:	4597	ck:	SW:TRAM_AGRT6
mus musculus (mouse). t	070548	μ	finds:	167	len:	5613	ck:	SW:TELT_MOUSE
homo sapiens (human). t	1 015273	μ.	finds:	167	len:	3375	ck:	SW:TELT_HUMAN
homo sapiens (human). t	1 P36402	1	finds:	269	len:	5007	ck:	SW:TCF1_HUMAN
chlorella virus il-3a (P52283	_	finds:	278	len:	7233	ck:	SW:T2C1_CHVI3
rattus norvegicus (rat)	P50235	_	finds:	285	len:	800	ck:	SW:SUH3_RAT

SW:YABP_EC	SW:YA32_PS	SW:Y988_METJA	SW:Y953_MY	SW:Y79B_METJA	SW:Y788_BC	SW:Y70A_ME	SW:Y503_ME	SW:Y4TG_RHISN	SW:Y4EK_RHISN	SW:Y464_MYCPN	SW:Y464_MYCGE	SW:Y425_MY	SW:Y373_TF	SW:Y280_MYCGE	SW:Y209_MYCPN	SW:Y209_MY	SW:Y040_HU	SW:Y021_NF	SW:WNT4_DF	SW:WN11_MC	SW:WN11_HUMAN	SW:WN11_COTJA	SW:WN11_CHICK	SW:VRPR_SALTY	SW:VRPR_SALDU	SW:VP8_BPPH6	SW: VMEM_PVMR	SW:VMEM_LVX	SW:VMEM_CVB	SW:VMA2_ORSVW	SW:VMA2_HRSVA	SW:VMA2_BRSVA	SW:VLF1_NF	SW:VID1_AG	SW:VID1_AGRT5
ECOLI c	PSEAE C		_мусти с		вокви с	метла с	_МЕТЈА С				CGE ck	_МУСРИ с	TREPA C			MYCGE C	_HUMAN c	NPVOP c	DROME c	MOUSE c													NPVOP c	AGRT6 c	
ck: 98	ck: 6657	ck: 9981	ck: 883	ck: 2865	ck: 1619	ck: 4119	ck: 6767	ck: 6923	ck: 5477	ck: 5866	k: 2836	ck: 2944	ck: 4876	ck: 9511	ck: 6533	ck: 590	ck: 4815	ck: 562	ck: 8394	ck: 1689	ck: 3073	ck: 4030	ck: 4630	ck: 7032	ck: 7061	ck: 6252	ck: 3415	ck: 8138	ck: 566	ck: 6559	ck: 9828	ck: 6337	ck: 889	ck: 4145	ck: 2312
len:	len: 1	len:	len:	len: 1	len: 4	len: 1	len: 4	len: i	len: 2	len: :	len: 3	len: 4	len: 4	len:	len:	len:	len: :	len:	len:	len:	len:	len: 3	len:	len: 3	len:	len:	len: 1	len:	len: :	len:	len: :	len: :	len:	len:	len:
216	122	329 .	282	170	440	102	406	231	248	385	385	450	477	265	309	308	153	298	389	354	354	354	354	297	297	149	109	108	106	186	194	186	374	147	147
finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:	finds:
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P39220	P21485	Q58395	P71557	P81233	051728	P81311	Q57926	P55661	P55434	P75112	P47702	P75172	083388	P47522	P75485	P47451	Q15053	010280	P40589	P48615	096014	P51891	P49339	P13041	P24417	P07579	P17527	P27331	P37989	Q84132	P04545	P29792	010330	P06667	P18591
escherichia coli. hy	pseudomonas aerugino	methanococcus jannas	mycobacterium tuberc	methanococcus jannas	borrelia burgdorferi	methanococcus jannas	methanococcus jannas	rhizobium sp. (strai	rhizobium sp. (strai	mycoplasma pneumonia	mycoplasma genitaliu	mycoplasma pneumonia	treponema pallidum.	mycoplasma genitaliu	mycoplasma pneumonia	mycoplasma genitaliu	homo sapiens (human)	orgyia pseudotsugata	drosophila melanogas	mus musculus (mouse)	homo sapiens (human)	coturnix coturnix ja	gallus gallus (chick	salmonella typhimuri	salmonella dublin. v	bacteriophage phi-6.	potato virus m (stra	lily virus x. hypoth	chrysanthemum virus	ovine respiratory sy	human respiratory sy	bovine respiratory s	orgyia pseudotsugata	agrobacterium tumefa	agrobacterium tumefa

	i p77396 escherichta corr. 11800	finds: 1	len: 285	ck: 4986	SW:YPDC_ECOLI
	bacillus subcilis.	finds: 1	len: 238	ck: 2171	SW:YOXD_BACSU
	caenorhabartis erey	finds: 1	len: 161	ck: 9212	SW:YOTC_CAEEL
	thermoproceus	finds: 1	len: 232	ck: 9154	SW:YORL_TTV1
.	caenornaburus	••	len: 381	ck: 431	SW:YNU6_CAEEL
L	34542 Caenornaburcis	••	len: 336	ck: 399	SW:YNC9_CAEEL
	34496 caenornaburces		len: 170	ck: 5825	SW:YNA1_CAEEL
		••	len: 139	ck: 7226	SW:YNO6_YEAST
×H		•	len: 69	ck: 7679	SW:YM27_MARPO
				CK: 8141	SW:YKFF_ECOLI
L	p75677 escherichia coli. hypot				
	i P46989 saccharomyces cerevisia	finds: 1	len: 196	ck: 8234	
	p39430 enterobacter aerogenes	finds: 1	len: 54	ck: 4167	
	P39411 escherichia coli. Nypou	finds: 1	len: 173	ck: 3873	SW:YJJX_ECOLI (
_		finds: 1	len: 317	ck: 1836	SW:YJ96_MYCTU
	mycobacterium	finds: 1	len: 164	ck: 7074	SW:YI29_MYCTU c
	escherichia cu	finds: 1	len: 197	ck: 1678	SW:YHGN_ECOLI c
	Saccitatomyces	finds: 1	len: 429	ck: 5569	SW:YHG3_YEAST C
_	pacifics subcition	finds: 1	len: 302	ck: 1929	SW:YHCT_BACSU c
	crypnonec	finds: 1	len: 319	ck: 3269	SW:YHA1_CRYPA c
	streptomyces c	finds: 1	len: 66	ck: 9954	SW:YGLR_STRCO C
	saccharomyces	finds: 1	len: 107	ck: 6897	SW:YGK9_YEAST C
	pacteriophage sport	finds: 1	len: 148	ck: 7782	SW:YG29_BPSP1 cl
H.	mycobaccerrum	finds: 1	len: 148	497	SW:YF58_MYCTU ck:
	saccharomyces	finds: 1	len: 128	5798	SW:YER4_YEAST ck:
Ď		finds: 1	len: 344	3748	SW:YDTG_SCHPO ck:
1	schizosaccharomyces	finds: 1	len: 174	8869	SW:YDSA_SCHPO ck:
	schizosaccharomyces	finds: 1	len: 131	6054	SW:YDM1_SCHPO ck:
	-	finds: 1	len: 317	1969	SW:YCQ5_YEAST ck:
	- 0	finds: 1	len: 299	51	SW:YCJZ_ECOLI ck:
	. 100	finds: 1	len: 262	6021	SW:YCJI_ECOLI ck:
	escherionia coii.	finds: 1	len: 78	1943	SW:YCGZ_ECOLI ck:
	escherichia coli.	finds: 1	len: 182	3224	SW:YCBQ_ECOLI ck:
	porphyra purpurea.	finds: 1	len: 291	4681	SW:YC38_PORPU ck:
	occus janna	finds: 1	len: 299	2920	SW:YC21_METJA ck:
	! Q48454 klebsiella pneumoniae	finds: 1	len: 373	4280	SW:YC08_KLEPN ck:
	O31458 bacillus subtilis. hypo	finds: 1	len: 249	3388	SW:YBFT_BACSU ck:
	O)	finds: 1	len: 192	2127	SW:YBCC_RHOCA ck:

SW	WS	WS	WS	WS	WS	WS	SW:	: WS	: WS	SW:	
SW:ZRP4_MAIZE	SW:YYVP_CAEEL	SW:YWFF_BACSU	SW:YU73_MYCTU	SW:YRKG_BACSU	SW:YRBC_HAEIN	SW:YR7B_ECOLI	SW:YQEK_ECOLI	SW:YQCE_ECOLI	SW:YPQQ_KLEPN	SW:YPJG_BACSU	
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ck: 6645	ck: 1176	ck: 3644	3649	ck: 1724	ck: 1216	ck: 6140	ck: 8893	ck: 1867	ck: 9681	ck: 3316	
len:	len:	len:	len:	len: 36	len: 214	len: 169	len: 141	len: 425	len: 271	len: 224	
: 364	len: 274	len: 394	len: 118	36	214	169	141	425	271	224	
finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	finds: 1	
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P47917	Q93834	P39642	P95085	P54434	P45028	P21316	P77136	P77031	P27509	P42981	
p47917 zea mays (marze). O	4 caenornabultis elega	2 bacillus subtilis. n	p95085 mycobacterium tuberc	P54434 bacillus subtilis. n	p45028 haemophilus influenz	P21316 escherichia coii. Hy	P77136 eschericnia coii. "Y	p77031 escherichia coli. ny	P27509 klebsiella pneumonia	p42981 bacillus subtilis. h	

Databases searched: SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999

Total finds: 37
Total length: 29,864,866
Total sequences: 82,229
CPU time: 03:12.78

FINDPATTERNS on Swiss-Prot: * allowing 0 mismatches

AAKG_PIG ck: 8859 len: 133 ! 009138 sus scrofa (pig). 5'-amp-activate :: <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{75}(A)x(P)(Y)xx(Y)(S)(K)xx(V)xxx(A)x(42)
LVYFDTSLQVKSALVQIYELEEHKXPVIDPESGNTLYILIXKLFITEFPKPEFMSKSLEELQI</pre>

ACP_BACSU ck: 8148 len: 77 ۳. <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x(A)x(T)(L)xx(V)(T)(K)xx(V)xxx(G)x(60)
MADTLERVTKIIVDRLGVDEADVKLEASFKEDLGADSLDVVELVMELEDEFDMEISDEDAE</pre> ! p80643 bacillus subtilis. acyl carrier p

- (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) x(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) x(1,2,2)(1,2,2 ADH2_DROMO ck: 8528 len: 253 | p09369 drosophila mojavensis (fruit fly)

ALR_TREPA ck: 255 len: 357 ! Q56346 treponema pailidum. alanine racem

AMIA_SALTY ck: 5663 len: 289 1 p33772 salmonella typhimurium. probable

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1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(A)XxX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)X(B,A)XXX(A)XX(B,A)XXX(A)XX(B,A)XXX(A)XX(B,A)XXX(A)XX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XXX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,A)XX(B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{9)}(P)X(P)X(P)X(A)XXX(G)X(254)

MSIRSNEVRLLKKQVNITKLOKKCSHSVAVIGAPESKGQKRRGVEHGPAAIRSAGLIDRLSNLGCN
PPIPGESWAKPCLSKSDIVYIGLRDLDPAGOFILKNYNISYYSWRHIDDMGIRRVM
EKTFDQLLGRRDRPIHLSFDIDAFDPALAPATGTPVIGGLTYREGVYITEEIHNTGMLSALDLVEVNPVLATTSEEVKATANLAVDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTTSSDKEIT
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MSTFKLLKTLTSRRQVLKTGLAALTLSGMSHAVAKEETLKTSNGHSKPKTKKTGSKRLVMLDPGHG
ATDRDHLLQQVLFDLVQTDTIKNSLTLGSHIKKIKPHKLHSRTTEQAAFVVLKS
PSIPSVLVETSFITNPEEERLLGTTAFRQKIATAIANGIISYFHWFDNQKAHTKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARG1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARG3_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANX2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPD_CITER
                                                                                                                                                                                                                      AT93_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARGC_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMPC_SERMA
<(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x[23](P)x(S)(A)xx(L)(S)(R)xx(A)xxx(G)x{103}
MFACAKLACTPSLIRAGSRVAYRPISASVLSRPEASRTGEGSTVFNGAQNGVSQLIQREFQTSAIS</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 6342 len: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 4724 len: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4641 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4321 len: 360
                                                                                                                                                                                                                      ck: 2178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 6452 len: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <(x)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M)(x\{164\}(P)x(P)(A)xx(W)(S)(R)xx(A)xxx(T)x\{7\}\\ \texttt{MLLENGWLVDARHVPSPHHDCRPEDEKPTLLVVHNISLPPGEFGGPWIDALFTGTIDPDAHPFFA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 4831 len: 187
                                                                                                                                                                                                                      len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            len:
                                                                                                                                                                                                                      142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Q91555 xenopus laevis (african clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P11446 escherichia coli. n-acetyl-gamma-gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! P24801 xenopus laevis (african clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Q00831 citrobacter freundii, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P18539 serratia marcescens. beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Q91554 xenopus laevis (african clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Q91553 xenopus laevis (african clawed
                                                                                                                                                                                                                      P48201
                                                                                                                                                                                                                homo
                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enteroba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BPHB_PSEPS
                                                     BR3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMPB_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMPA_XENLA ck: 9714 len: 398 ! P25703 xenopus laevis (african clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>..</u>
                                                           ck:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 1527 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 1620 len: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \(\lambda\) \(\lam
                                                           2610
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len: 423

! Q01851 homo sapiens (human). brain-speci

1 P30884 xenopus laevis (african

clawed

fr

! P08694 pseudomonas pseudoalcaligenes.

ŭ

	ATP8_PODAN	ck: 8763 len: 50 ! Q02653 podospora anserina. atp synthase
	1:	<pre><(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{20}(A)x(T)(V)xx(L)(S)(K)xx(L)xxx(V)x{14} mpQLVPfYFVNEITFTFIILAITVYILSKYILPRFVRLFLSRTFISKLLG</pre>
	ATP8_PONPA	ck: 3336 len: 68 ! P92694 pongo pygmaeus abelil (sumatran o
	::	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W x{34}(P)x(T)(P)xx(F)(T)(K)xx(L)xxx(P)x{18} MPQLNTTTMPTIITPMLLALFLITQLKLLNSHLHPPTPPKFTKPKLHAKPWGPKWTKVYLP</pre>
	ATP8_PONPP	ck: 3460 len: 68 ! P92896 pongo pygmaeus pygmaeus (bornean
1	1:	<pre><(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W x{34}{P}x(T)(P)xx(F)(T)(K)xx(P)xxx(P)x{18} MPQLNTTTWLTIITPTLLALFLITQLKLLNSHLHPPTPPKFTKTKPHAKPWELKWTKIYSP</pre>
	ATP8_PONPY	ck: 3550 len: 68 ! Q35584 pongo pygmaeus (orangutan). atp s
		<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{34}(P)x(T)(P)xx(F)(T)(K)xx(P)xxx(P)x{18} MPQLNTTTWLTVITPTLLALFLITQLKLLNSHLHPPTPPKFTKTKPHAKPWELKWTKIYSP</pre>
	ATPD_HUMAN	ck: 1686 len: 168 ! P30049 homo sapiens (human). atp synthas
	:	<pre><(X){1,200}(L,I,V,M,A,F)X(F,T,S)(L,I,V,M,A,F)XX(L,I,V,M,A,F,Y,W x{141}(V)x(T)(A)xx(A)(T)(R)xx(I)xxx(I)x{11} MLPAALLRRPGLGRLVRHARAYABAAAAAAAASGPNOMSFTFASFTQVFFNGANVRQVDVPTL</pre>
	ATPZ_BACP3	ck: 4392 len: 127 ! P09354 bacillus ps3 (thermophilic bacter
		<(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)

1: MKRKDIFFOKLNELISNAYVPYSNERVSCLLLTDGGWFAGVNLENSALSELLCALLANDERS ALGARIAN CK: 8973 len: 288 ! P44937 haemophilus influenzae. phosphatidat cdsa_haein ck: 8973 len: 288 ! P44937 haemophilus influenzae. phosphatidat cdsa_haein ck: 8973 len: 288 ! P44937 haemophilus influenzae. phosphatidat cdsa_haein ck: 8973 len: 288 ! P44937 haemophilus influenzae. phosphatidat cdsa_haein ck: 1.7, v, M, A, P)XX(L, I, V, M, A, F, Y, W)(C <	CDD_BACSU ck: 9048 len: 136 p19079 bacillus subtilis. cytidine deaminas <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) 1 x(81)(P)x(S)(P)xx(A)(C)(P)xx(I)xxx(C)x(39) 1: MNRQELITEALKARDMAYAPVSKEQVGAALLTKDGKVYRGCNIENAAYSMCNCAERTALFKAVSEQ 1: MNRQELITEALKARDMAYAPVSKEQVGAALLTKDGKVYRGCNIENAAYSMCNCAERTALFKAVSEQ CDD_MYCPI ck: 6718 len: 133 p47718 mycoplasma pirum. cytidine deaminase CDD_MYCPI ck: 6718 len: 133 p47718 mycoplasma pirum. cytidine deaminase <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(83)[1)x(T)(P)xx(V)(C)(R)xx(L)xxy(A)x(34) x(83)[1)x(T)(P)xx(V)(C)(R)xx(L)xxy(A)x(34)	CAMG_MOUSE ck: 283 len: 294 ! P49070 mus musculus (mouse). calcium-signal <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) ((X){1,38}(A)x(P)(A)X(A)(B)(B)XX(L)XX(L)XX(L)X(L,I,V,M,A,F,Y,W)(C) MEDVPAATDGGERPATPSGLSASORABLERREKLIMNGEDRINRINGFHRPGSGSEEENQTKSKPQ STAEEFDSFRIFRLYGGALLALGVRAPYCKYLSIFAPSTITLOLAYMGLYKYFPKGE STAEEFDSFRIFRLYGGALLALGVRAPYCKYLSIFAPSTITLOLAYMGLYKYFPKGE KKYKTTYLTAALLLSGIPAEAINRSMDTYSKNGEVFTDLCVYFFTFIFCHELLDYMGPEVP KKYKTTYLTAALLLSGIPAEAINRSMDTYSKNGEVFTDLCVYFFTFIFCHELLDYMGPEVP	CAD1_DICDI ck: 3813 len: 213 i p54657 dictyostelium discoldeum (slime mold cAD1_DICDI ck: 3813 len: 213 i p54657 dictyostelium discoldeum (slime mold c(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(Y)XXX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(L,I,V,M,A,F,Y,W))(Q x(Y)XX(A)X(A)X(A)X(A)X(A)X(A)X(A)X(A)X(A)X(LOTHTRAETOFIAVTAK/ONEELITALK KHMF FARAE LICKUMINESAPYPHPYORSSPPTNYGHDTAASLPMMPTHDNWSGLEVS I PQESQLGGWFLPGTGPICPPPNPHOFAPSLGLPSHGCDRYSTLRNHRSAPYPHPYORSSPPTNYGHDTAASLPMMPTHDNWSGLEVS I P33967 bacillus cereus. blasticidin-s deami BSR_BACCE ck: 8425 len: 140	SMEDICODOPCY SOLD-WRE LFG-NOT-LOCAL PRADE CARE TO A STATE CARE		<pre><(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q)</pre>
1 (A) (L) (A) (L) (A) (T) (R) (X) (Y) (XXX (S) X (196) (XXX (S) X (196) (YXX (S) X (L, I, V, M, A, P) X (P, T, S) (L, I, V, M, A, P) X (E, I, V	COBT. 1 NNTTPAAAIVSTI VLAKVGGFDLVGI COX3	. 5 . 5	COAT_TCV ck: 1818 len: 351 PO6663 turnip crinkle virus (tcv). Coat_ (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) (X){49}(A)X(P)(Y)X(V)(P)(R)XX(L)X(287) MENDFRYRKPASDGAOMALKWQKKOWSTLTSROKOTARAMGITLSPVAQPVQKVTRLSAPVA 1: MENDFRYRKPASDGAOMALKWQKKOWSTLTSROKOTARAMGITLSPVAQPVQKVTRLSAPVA SVPWTGFILTVPTDSTDRFVADGISDFKVDFGKLIMATYGOGANDAQLGEVRVE SVPWTGFILTVPTSSTDAQIGDFAGVKDGPRLVSWSKTKGTAGWEHDCHFLGTGNFSLTLFYEKAPVSGLENADASDFSVLGEAAAGS YTVQLKNRTGSTSDAQIGDFAGVKDGPRLVSWSKTKGTAGWEHDCHFLGTGNFSLTLFYEKAPVSGLENADASDFSVLGEAAAGS	DAVGGSLMEETAPVAL	P	schizosaccharomyces postacki syllivy, M.A.P)XX(L,I S)(L,I,V,M,A,P)XX(L,I cx(L)xxx(S)X[27] SHIKLNTOVPAPFKAVDNINOO SHIKLNTOVPAPFKAVDNINOO MLLDFDISWPGPMSFLRRISRA	1 <pre><(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,E,Y,W)</pre>

CDSN_PIG

```
(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,x(L))(S)(H)xx(A)xxx(M)x(211)
x(196](M)x(S)(L)xx(L)(S)(H)xx(A)xxx(M)x(211)
mMSMNSKQPHFAMHPTLPEHKYPSLHSSSEAIRRACLPTPPIQSNLFASL
1:
mMSMNSKQPHFAMHPTLPEHKYPSLHSSSEAIRRACLPTPPIQSNLFASL
GGGGPGGGLLGGSAHPHPHMHSLGHLSHPAAAAAMNRPSGLPHPGLVAAAAHHGAA
AAAAAAAAAAAAVVGAAGLASICDSDTDPRELEAFAERFKQRRIKLGVTQADVGSALANLKIPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX()
x(79)(L)X(S)(I)XX(L)(S)(K)XX(V)XXX(A)X{118}
MSYDANKVKFEFGKNCTGESFEXNKGETVRENNGDKNNDKEMSCLVGS)
1: MSYDANKVKFEFGKNCTGESFEXNKGETVRENNGDKNNDKEMSCLVGS)
1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(
x(138)(A)x(P)(A)xx(A)(S)(H)xx(L)xxx(L)x1140)
mepypaatdggerpatpsglsasgraellarkinnsegrinringe
ftaeefdsfrifrlyggallalgyrafygkylsifaffttlglaynglykyfpkge
kkykttvltaalllsgipaeainrsmdtyskngeyftdlcvyfftfifcheildymgpeyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRA1_BRAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRA2_BRAFL
                                                                                                                                                                                                                                                                                CAD1_DICDI
                                                                                                                          CAMG_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                    BSR_BACCE
                                                                                                                                                                                                                                                                                                                                          1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 7365 len: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ck: 391
                                                                                                                                                                                                                                                                                                                                          <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(I
x{95}(V)x(S)(P)xx(M)(C)(R)xx(I)xxx(A)x{29}
MKTFNISQQDLELVEVATEKITMLYEDNKHHVGAALRTKTGEIISAVH)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 8425 len: 140 ! P33967 bacillus
                                                                                                                                                                                                                                                                                     ck: 3813 len: 213
                                                                                                                            ck: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len: 440
                                                                                                                                 len: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! Q17134 branchiostoma florio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! P80492 branchiostoma flori
                                                                                                                                                                                                                                                                                            ! P54657 dictyostelium disc
                                                                                                                                      i p49070 mus musculus (mous
                                                                                                                                                                                                                                                                                                                                                                                                                                    cereus. bl
```

ERSKGVILNISSASGMLPVPLLTIY LVATKLAKIQKPTLDKPSAETFVKS <i>i</i>	1
1 <(X)	DACX_STRSK ck: 4817 len: 291 ! P39042 streptomyces sp. (strain k15). d-ala
NISSGYCYRPWPLYSLYSASKAFYCT YLNTSRYTKTADEFYKESLKYYTIG DHBK_MOUSE Ck:	(X){1.200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)x(2)} x(192){1,x(S)(A),x(A)(T)(R)xx(I)xxx(C)x(91)} x(192){1,x(S)(A),x(A)(T)(R)xx(I)xxx(C)x(91)} x(11)xxx(I)xxx(I)xx(I)xx(I)xx(I)xx(I)xx(
1 <(X) x{ 1: MEQE	CYNR_ECOLI ck: 4304 len: 299 ! P27111 escherichia coli. cyn operon transcr
DHB3_RAT ck:	1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(64)(P)x(P)(A)xx(V)(T)(K)xx(A)xxx(V)x[12] 1: ADESALAQTKGCLACHNPEKKVVGPAYGWVAKKYAGQAGAEAKLVAKVMAGGQGVWAKQLGAEI
1: NISSGAALRPWPLYSLYSASKAFVYI YLNNKMTKTADEFVKESLKYVTIGAE	'CY2_RHOTE ck: 2620 len: 92 ! P00098 rhodocyclus tenuis (rhodospirillum t
DHB3_MOUSE ck: (X)	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x{103}(I)x(P)(L)xx(Y)(S)(H)xx(Y)xxx(Y)x(B) 1: QAVLYPSIYSILSKSKVRVQELEPVEGAAVPADTKKAEIKEKEHEVITHGLPVPYSSVVQPIVS
AMEKYENENVIEKTADEFYKESINYV	CU04_BLACR ck: 1926 len: 127 ! P80675 blaberus craniifer. cuticle protein
DHB3_HUMAN ck: 1 <(X) 1; MGD GLILNISSGIALFPWPLYSMYSASKA	<pre>1</pre>
	CTAA_BACSU ck: 1522 len: 306 ! pl2946 bacillus subtilis. cytochrome aa3 cc
DHAT_KLEPN ck: <(X) X X ASY I: MSYP INDPLIMIGEPAALTAATGMDALTHA AVALGSNIOARPHMAYASILAGMAPH AVALGSNIOARPHMAYASILAGMAPH	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(Y)(X)(Y)(X)(X)(Y)(X)(Y)(X)(Y)(X)(Y)(X)(Y)(X)(Y)(X)(Y)(X)(Y)(X)(X)(X)(X)(X)(X)(X)(X)(X)(X)(X)(X)(X)
	CTAA_BACFI ck: 716 len: 297 ! Q04443 bacillus firmus. cytochrome aa3 cont
DHAT_CITER ck: (X) X(1: NOTE: NOTE: NOTE: AVALGENTA AT SALAGMAPP AVALGENTA AT SALAGMAPP	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X){1,201} x{24}(A)X(S)(V)XX(A)(T)(R)XX(V)XXX(I)X(291) mASLKDVARLAGVSMMTVSRVMAESVRATBRVLQAIQTLNYVPDLSARKMRAQGRKPSTLAV RQPLCFWLPESALATGYRRQGFEQAWRDAGRDLAGVKQFHAATGDDHYTDLASLLN RQPLCFWLPESALATGYRRQGFEQAWRDAGRDLAGVKQFHAATGDDHYTDLASLLN AHFKSGKPDFDVLICGNDRAAFVAYQVLLAKGVRIPQDVAVMGFDNLVGVGHLFLPPLTTIQLPHDIIGREAALHIIEGREGGRVTRI
. 1: MTK#	CSCR_ECOLI ck: 8969 len: 331 ! P40715 escherichia coli. sucrose operon rep
DFP_STRMU ck: 1 <(X)	x(85)(Y)x(P)(V)xx(P)(S)(R)xxx(A)xxx(G)x(301) HESRYLSRATTLSSLPTLUKLHRLPLAMASLPSYKSFGSVSDGGNLVWGRQLRPELCSPYLKKGAS TSNVSFAAVAVSFTHTVKALEPFFNAAASQFILGQSIPITLHLSLAPVVIGVSMAS LTELSFNWLGFISAMISNISFTYRSIYSKKAMTDWDSTNIYAYISIALIYCIPPALIIEGPTLLKTGFNDAIAKVGLVKFVSDLFWV
1: TLEVVQEMGKFTKITSQLIVPDSFEK KIFVLDEADNMLDQQGLGDQCIRVKK	CPTR_PEA ck: 5889 len: 402 ! P21727 pisum sativum (garden pea). triose p
DBP5_YEAST ck: <(X) x(1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(54)(P)xx(P)Xx(V)(S)(H)xx(A)xxx(S)x(44) 1: QVGYSGIVSPDGNNIQFTHDFAHSIVLKGPSGIVTSDGKNLQLTAGQASLQAAAPAPPLPVSHY
ANYSTPRHLTKIASSAMKNSTFRTVV SYSGAIGVKTGSGPEAKYCLVFAATF	CPC1_CANPG ck: 1605 len: 114 P81580 cancer pagurus (rock crab). cuticle

/VKTKAYTAKTVTKTGSIRTMDTWKNTNGLLS TRGGKTVIGTVLASTSIPARESDATKIMNYGFAL

DBP5_YEAST ck: 2958 len: 482	
ck:	
2958	
len:	
482	
P20449	
P20449 saccharomyces cerevisiae (baker's	
cerevisiae	
(baker's	

X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X;146](A)x(S)(L)xx(L)(T)(R)xx(P)xxx(S)x{320}
DTKRDPADLLASLKIDNEKEDTSEVSTKETVKSQPEKTADSIKPAEKLVPKVEEKKTKQED
EKNKQINAQVIYGTPGTVLDLMRRKLMQLQKI
KRFLPKDTQLVLFSATFADAVRQYAKKIVPNANTLELQTNEVNVDAIKQLYMDCKNEADKF

9135 len: 145 ! Q54433 streptococcus mutans. dna/pantoth

X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{45}(P)x(T)(L)xx(L)(S)(K)xx(V)xxx(V)x{84} KKILLAVSGSIAAYKAADLSHQLTKLGYHVNVFMTNAAKQFIPPLTLQVLSKNPVYSNVMK

len: 387 ! P45513 citrobacter freundii. 1,3-propane

X)[1,200](L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W,X;[143](A)x(T)(A)xx(V)(T)(R)xx(V)xxx(T)x[28]
xRMFDYLVPNVNFFGPNAISVVGERCKLLGGKNALLVTDKGLRAIKDGAVDKTLTHLREAG
HAVBAYISKDANFYTDAAAIQAIKUIARNURQ
FNNANLGYVHAMAHQLGGLYDMPHGVANAVLLPHVARYNLIANPEKFADIAEFMGENTDGL

846 len: 387 ! Q59477 klebsiella pneumoniae. 1,3-propan

X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X;[143](A)x(T)(A)xx(V)(T)(R)xx(V)xxx(T)x(228]
xRMFDYLVPNVNFFGPNAISVVGERCQLLGGKALLVTDKGLRAIKDGAVDKTLHYLREAG
HAVEAYISKDANFYTDAAANQAIRLIARNURQ
FNNANLGYVHAMAHQLGGLYDMPHGVANAVLLPHVARYNLIANPEKFADIAELMGENITGL

3434 len: 310 ! P37058 homo sapiens (human). estradiol 1

X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,[193](L)x(S)(M)xx(A)(S))(K)xx(V)xxx(S)x[101]
DVLEQFFILIGLLVCLACLAKCVRESRCVLLNYWKVLPKSFLRSMGQWAVITGAGDGIGKA
KAFYCAFSKALQEYKAKEVIIQVLTBYAVST
YVTIGGETCGCLAHEILAGFLSLIPAWAFYSGAFQRLLLTHYVAYLKLNTKVR

9317 len: 305 ! P70385 mus musculus (mouse). estradiol 1

X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X(189](L)x(S)(L)xx(A)(S))(R)xx(V)xxx(S)x(100]
KLFIAAGLFVGLVCLVKCMRFSQHLFLRFCKALPSSFLRSMGQWAVITGAGDGIGKAYSFE
YTFSKALSVEYRDKGIIIQVLTPYSISTPWTK
AESCGCLAHEIIAIILNRIPSRIFYSSTAQRFLLTRYSDYLKRNISNR

3366 len: 306

! 054939 rattus norvegicus (rat). estradio

X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{189}(L)x(S)(L)xx(A)(S)(K)xx(V)xxx(S)x{101} QFLLSVGLLVCLVCLVKCVRPSRYLFLSFCKALPGSFLRSMGQWAVITGAGDGIGKAYSFE

;TFSKALNVEYRDKGIIIQVLTPYSVSTPMTK ;AETCGCLAHEILAIILNLIPSRIFYSSTTQRFLLKQFSDYLKSNISNR

4788 len: 312 ! 070503 mus musculus (mouse). putative st

X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)15]
X(151](V)x(S)(V)xx(V)(T)(R)xx(L)xxx(V)x(135)
CAPPAAGELYMVGASTIAYLALRASYSLERAFQVCVGNEALVGPRLGEWAVVTGGTDGIG
YSATKAFVDFFSQCLHEEYKSKGIFVQSVMPY SAIKTVGLQTRTTGYVIHSLMGSINSIMPRWMYFKIIMGFSKSLRNRYLKKRKKN

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LTKALGLELARTGITVNAVCPGFVETPMERKVERHYAGINGVSSEETFDRITINKVP LGRYVETREVAANVEYLVADDAAVTAQALNVCGGLGNY LGRYVETREVAANVEYLVADDAAVTAQALNVCGGLGNY DHKR_STRCM ck: 4473 len: 261 ! P41177 streptomyces cinnamonensis. monensin ck: 4473 len: 261 ! P41177 streptomyces cinnamonensis. monensin DHKR_STRCM ck: 4473 len: 261 ! P41177 streptomyces cinnamonensis. ck: 11,200 (L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M)(C) 1	DHCA_RAT ck: 3202 len: 276	1 P47844 OFFCCLEGUS CHIEFER (X,A,F)X(L,I,V,M,A,F,Y,A,F)X(P,T,S)(L,I,V,M,A,F)X(L,I,V,M,A,F,Y,A,V)X(P)(K)XK(V)XXX(S)X(72) A_TRALCRIESCBUPLITAQDEAQGQAAVQQLQAEGLSPREHQLI SKILVNACCPGWVRTD EQW EQW TABLE TO THE COLUMN (Xat). Carbon	DHCA_MOUSE ck: 204 len: 276 ! p48758 mus musculus (mouse). carbonyl reduc <(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q) x(188](P)x(S)(A)xx(Y)(T)(X)xx(Y)XxX(S)x{72} x(188)(P)x(S)(A)xx(Y)(T)(X)xx(Y)XxX(S)X(72) SSSRVALVTGANKGIOFAITEDLCRKESGDVULAARDEERGOTAVQKLQAEGLSPRFHQLDIDNF 1: SSSRVALVTGANKGIOFAITEDLCRKESGDVULAARDEERGOTAVQKLQAEGLSPRFHQLDIDNF 1: TKKGYHAEEGWPNSAYGVTKIGVTULSRILARKLEERBEDKILLNACCPGWVRTD MAGPKATKSPEEGAETPVYLALLPPDAEGPHGQFVQDKKVEPW		1 reduc ,Y,W)(C	DHBX_ANAPL ck: 9157 len: 312 057314 anas platyrhynchos (domestic duck). <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(d) x{160}(1)xS(S)(V)xx(M)(T)(R)xx(L)xXx(L)x{136} x(160)(1)xG(S)(V)xx(M)(T)(R)xX(L)xXx(L)X(L)X(L)X(L)X(L)X(L)X(L)X(L)X(L)X(L)X
	VNLTNLAQSWRKPĒKNFGMQLELQVMHLMNMLHDHAYVQIPDLHAFLVV VSUKPELK CRSRRKRSASYYLPVTPSNVCKPRLYIDFKDVGWQDMIIAPQGYLANYCHGECPFPLSESLNGTNHAILQTLVHSFDPKGTPQP CRSRRKRSASYYLPVTPSNVCKPRLYIDFKDVGWQDMIIAPQGYLANYCHGECPFPLSESLNGTNHAILQTLVHSFDPKGTPQP CRSRRKRSASYYLPVTPSNVCKPRLYIDFKDVGWIAHPAHYCHGECPFPLSESLNGTNHAILQTLVHSFDPKGTPQP ### 1 ### 1	LSFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHYQYKSLFVEDNHKALL SSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMETNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPHCS SSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMETNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPHCS SSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMETNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQN (zebrafish) (ze DVR1_BRARE ck: 2951 len: 355	INVMEVGILDAGGLRALLREGAAVCULLUNGANG LATINGANG LEAGURALLEGAGURALLEGAGURA LET LYLGSAYHASRKDMLDALGITALLINVBANG DNHFEGHYQYKSIPVEDNHKADI SENGGLLQFESQVLAPHCS SSWENEAIDFIDSIKDAGGRVEVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKORRSIISPNFSFMGQLLQFESQVLAPHCS SSWENEAIDFIDSIKDAGGRVEVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKORRSIISPNFSFMGQLLQFESQVLAPHCS SSWENEAIDFIDSIKDAGGRVEVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKORRSIISPNFSFMGQLLQFESQVLAPHCS (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck: 6443 len: 367 Q64623 rattus norvegicus (rat). dual spe DUS1_RAT ck	1: NYMEYOTIDAGGIRALLGERAACJUANINGANGTICLAVIMETORYKSIPVEDNIKADI LPETYIGSAYHASRKDMIDALGITALINVSANCPNIEGEHYCYKSIPVEDNIKADI SSWENEAIDEIDSIKNAGGRVFVHCQAGISRSATICLAYIMETNRVKLDEAFEETVKQRRSIISPNFSFMGQILQFESQVLAPHCS SSWENEAIDEIDSIKNAGGRVFVHCQAGISRSATICLAYIMETNRVKLDEAFEETVKQRRSIISPNFSFMGQILQFESQVLAPHCS SSWENEAIDEIDSIKNAGGRVFVHCQAGISRSATICLAYIMETNRVKLDEAFEETVKQRRSIISPNGQLIQFESQVLAPHCS DUS1_MOUSE ck: 5871 len: 367 ! p28563 mus musculus (mouse). dual specif DUS1_MOUSE ck: 5871 len: 367 ! p28563 mus musculus (mouse). dual specif \$\(\) \(\	1	DLTE_BACSU ck: 2631 len: 252 ! p39577 bacillus subtilis. dlte protein. (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) (X){1,270}(V)X(A,F)(V)XX(A,F)X(E)XXX(S)X(B) (X){1,47}(V)X(P)(V)XX(A,F)X(E)XXX(S)X(B) (X)X(E)XXX(S)X(B) (X)X(E)XX(E)XXX(E)XX(E)XE (X)X(E)XX(E)X

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1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,I,V,W,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,A,F,Y,W)(C,I,V,M,X,I)XXXX(M)X(I18)

1: MNLEGKIALVTGASRGIGRAIAELLVERGATVIGTATSEGGAAAISEYLGENGKGLALNVTDVESI
TVAPGFIETDMTKALNDDQRAATLSNVPAGRLGDPREIASAVVFLASPEAAYITGE
TLHVNGGMYMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESRLTWLSILIIIIIAVISIAQVLLIQFLFTGRQKNYV
FENR_ECOLI
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   <u>с</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x{33}(M)x(T)(M)xx(L)(T)(H)xx(P)xxx(P)x{95}
mafgsmnssddspmsdinvtplvdvmlvllivfmitmpvlthsiplelptaseqankqdkqpkdpl</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ck: 3764 len:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ck: 4159 len: 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 1627 len: 270
                                                                                                                                                                                                                                                                                                                           ck: 5984
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   len:
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247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! O54438 pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! P43713 haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P95376 neisseria meningitidis. biopolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! 006434 neisseria gonorrhoeae. biopolymer
! P28861 escherichia coli. ferredoxin--nadp
                                                                                                                                                                                                                                                                                                                           ! P55336 vibrio harveyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! 033096 mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! Q90257 brachydanio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leprae.
                                                                                                                                                                                                                                                                                                                           3-oxoacyl-[acyl-carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (zebra
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1 <\(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)}(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)}
1: ADWYTGKYTKYONWTDALESLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLE
GSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLLKETRQMTKH
LRRRPGHMTAEHYM
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FENR_SHIFL ck: 1251 len: 135 ! P28901 shigella flexneri. ferredoxin--na

(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{29}(P)X(T)(A)XX(F)(T)(X)XX(G)XX(G)X{90}

1: MADWYTGKYTKVQNWTDALFSLTVHAPVLPETAGQETKLGLEIDGERVQRAYSYVNSPDNPDL
FIBR_AGKCO ck: 7566 len: 203 ! P28891 agkistrodon contortrix contortrix

(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,P)XY(L,I,V,M,A,P)XX(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F
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FIMH_SALTY ck: 6074 len: 335 | P37925 salmonella typhimurium. fimh prot <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,P)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)(L,I,V,M,A,R)X(P,T,S)

1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,WX(L,I,V,M,A,F,Y,WX(L,I,V,M,A,F,Y,WX(L,I,V,M,A,F,Y,WX(L)XXX(L)XXX(C)X{310} MXIYSALLLAGTALFTHPALATHNALTHOLFYDLSDVFTSGNNOPGQVVTLPEKSAWV DALSTPVYTISYSGKVEVPONCEVNAGQYVETPGDLGAS,LESQAAGURPOGUTP QTKTIAIKCTNVAAQAYLSMRLEAEKASGQAMVSDNPDLGFVVANSNGTPLTPNNLSSKIPFHLDDNAAARVGIRAWPISVTGIK

FGRVDASVDTQLMQLKDKLLTALEAGAAE FOS_AVINK ck: 9324 len: 322 ! P23050 avian retrovirus nk24. p55-v-fos

FOS_CHICK ck: 7007 len: 367 ! P11939 gallus gallus (chicken). p55-c-fo

1 <(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(99)(P)x(P)(P)xx(Y)xxx(P)x(252) 1: MMYQGFAGETEAPSSRCSASPAGDSLTYPSPADSFSSMGSPVNSQDFCTDLAVSSANFVPT LQAEIANLLKEKEKLEFILAAHREACKNPEELRRSEELAAATALDLGAPSPAAAEE AFALPLMTEAPPAVPPKEPSGSGLELKAEPFDELLFSAGPREASRSVPDMDLPGASSFYASDWEPLGAGSGGELEPLCTPVVTCT

FOS_HUMAN ck: 4677 len: 380 ! POll00 homo sapiens (human). p55-c-fos

FTRC_MAIZE ck: 4642 len: 152 ! P41347 zea mays (maize). ferredoxin-thio

<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)}

x{15}(V)x(P)(L)xx(A)(T)(R)xx(P)xxx(A)x{121}

ntstytttygcgglpyrplstatrgrprrcayradaagabasndksyevmrkfssgyarrsnt

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X(294) x(65;L)X(T)(A)XX(T)(S)(K)XX(T)XX(T)X(294) x(65;L)X(T)(A)XX(T)(S)(K)XX(T)XXX(T)X(294) MOKLOLCYYIYLEMLIVAGPVDLNENSEQRENVERBGLCNACTWRQNTKSSRIEAIKIQILSKLRIXDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN KPMKDGTRYTGIRSLKLDMNPGTGIWQSIDYKTYLQNWLKQPESNLGIEKALDEN GHDLAVTFPGPGEDGLNPELEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEALGWDWIIAPKRYKANYCSGECEFVFLQKY
                                                                                                                                                                                                                                                                                                                          <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(D,X,00)(V)x(P)(V)xx(F)(S)(R)xx(P)xxx(I)x(27)
x(80)(V)x(P)(V)xx(F)(S)(R)xx(P)xxx(I)x(27)
MYGKIIFVLLLSEIVSISASSTIEVAMHISTSSSVIKSYISSQINDKHKGDIYPATLGAHEVSE
MYGKIIFVLLLSEIVSISASSTIEVAMHISTSSSVIKSYISSQINDKHKGDIYPATLGAHEVSE</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i 008689 mus musculus (mouse). growth/differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! 014793 homo sapiens (human). growth/differ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i 018828 papio hamadryas (hamadryas baboon)
                                                                                                                                                                                                                                                                                                                                                                                                        ! O18831 sus scrofa (pig). growth/differenti
                                                                                                                                                                                                  O18830 ovis aries (sheep).
                                                                                                | Q28914 pan troglodytes (chimpanzee).
                     ; p37606 escherichia
                                                                                                                                                                                                                                                                                                      035312 rattus norvegicus (rat). growth/dif
,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
                          coli.
                          glycerol-3-phosph
                                                                                                                                                                                                          growth/differen
                                                                                                          glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x(68)(L)x(T)(A)xx(A)(S)(R)xx(L)x(X(P)x(255)

MNORNASMIVIGAGSYOTALAITLARNGHEVVLWGHDPEHIATLERDRCNAAFLPDVPFFDTL
RVYSNPDFIGVOLGGAVKNVIAIGAGMSDGIGFGANARFALITRGLAEMSRLGAAL
GADPATFMGMAGLGDLVLTCTDNOSKNRRFGMMLGOGMDVQSAQEKIGQVVEGYRNTKEVRELAHRFGVEMPITEEIYQVLYCGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)](P)xx(Y)(S)(K)xx(M)xxx(L)x(183]
x(97)(P)xx(P)(P)xx(Y)(S)(K)xx(M)xxx(L)x(183)
MHERESECREDOKPVMDDORDLISNNEQLEMCREPGAPESKCSEGALXTGFSILVTLLLAG
WKVFESWMHHWLLFEMSRHSLEQKPTDAPPKVLTKCQEEVSHIPAVPHGGSFRPKCD
ENGNYLPLQCYGSIGYCWCVFPNGTEVPNTRSRGHHNCSESLELEDPSSGLGVTKQDLGPVPM
                                                                                                                                                                           GPRD_HUMAN
                                                                                                                                                                                                                                                                                                                                                     HG2A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPRD_RAT
                                                                                                                                                                                                                                                     HIS8_SALTY
                                                                                                                                               HISO_ECOLI
                                                        HMPH_HUMAN
              ۲:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 2863 len: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ck: 4478 len: 354
                                                                                                                                                                                                                                                     ck: 516
                                                                                                                                                                                                                                                                                                                                                         ck: 9949 len:
                                                                                                                                                     ck: 7651
              len:
                                                                                                                                                      len: 228
                                                                                                                                                                                                                                                                                                                                                              296
                                                                                                                                                                                                                                                           359
                                                                 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; p35411 rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                p50200 clostridium sordelli.
                                                                                                                                                                                                                                                                                                                                                             ! P04233 homo sapiens (human). hla
                                                                                                                                                      ! P52094 escherichia coli. histidine trans
                                                                i Q03014 homo
                                                                                                                                                                                                                                                           P10369 salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens (human).
                                                                   sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (rat). probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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GDF8_BOVIN ck: 9403 len: 375 ! O18836 bos taurus (bovine). growth/differen

GDF8_HUMAN

ck: 1814

len:

375

GDF8_MOUSE

ck: 2293 len: 376

GDF8_PAPHA

ck: 1463 len: 375

ck: 1805 len: 375

GLPB_PANTR

ck: 149

len: 123

GDF8_RAT

ck: 1496

len:

376

ck: 1548 len: 375

GPDA_ECOLI

<(X){1,200}(L,I,V,M,A,P)X(P,T,

Page

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(103)(V)X(P)(V)XX(W)(S)(H)XX(L)XXX(S)X(193)
1: TLEMERLIQAKGGSESQNVEELLNLFKRGPQAFDAFCEALRETRGGHLEDLLLTTLSDIQHILPPL
DQTAQEMQEKLQNFAQLPAHRVTDSCIVALLSHGYEGGIYGVDGKLLQLGEVFELF
DNANCPSLQNKPKMFFIQACRGDETDRGVDQQDGKNHAQPPGCEESDTVKEELMKMRLPTRSDMICVYACLKDNAPIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C X{25}(P)X(T)(M)XX(L)(S)(R)XX(L)XXX(G)X(258)

1: AKVETKDVMEQFILELISGEEGINRPITMSDLSRPGIEIAGYFTYYPRERVQLLGKTELSFFEQLF
VEIRQEDQDTLYGNAPELIEHLLEIRGLGINYVTLFGAGAVRSNKRITIVMNLEL
WEQGKQYDRLGLEEETMKIIDTEITKLTIPVRPGRNLAVIIEVAAMNFRLKRMGLNAAEQFTNKLADVIEDGEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x[104](P)X(T)X(Y)(T)(H)XX(L)XXX(P)X(151) MOFPHEGPAAPAVGVLYAPTPLLOPAHPTPFYIDDILGRGPAAPTPTLPSPNSSFTSLVSSYSEROVKTWFQNRRAKWRRLKQENPQSNKKDALDSLDTSCEQGQDLPSEQNKGASLD RSQCSPSPASQEDPDSEISEDSDQEVDIEGDKGYFNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERQVKTWFQNRRAKWRRLKQENPQSNKKEELESLDSSCDQRQDLPSEQNKGASLDS
SQCSPSPASQEDLESEISEDSDQEVDIEGDKSYFNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYCD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUPK_RHILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPRK_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMPH_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                               IAA5_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAA2_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAA1_WHEAT
                                                                                                                                                                                                                                          ICE2_RAT
                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 1548 len: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ck: 4393 len: 309
                                                                                                                                                                                                                                                                                                       ck: 4073 len: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(91](A)x(S)(I)xx(V)(C)(R)xx(I)xxx(A)x(I7]
SGPWMCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSM</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ck: 3320 len: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 675 len: 307
                                                                                                                                                                                                                                          ck: 8827 len: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                           <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x{90}(A)x(S)(V)xx(V)(C)(K)xx(I)xxx(S)x{17}
SGPWSWCNPATGYKVSALTGCRAMVKLQCVGSQVPEAVLRDCCQQLADINNEWCRCGDLSSMLF</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 4825 len: 123
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d
                                         7697 len:
                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
                                         ! P10822 psophocarpus tetragonolobus (goa be
                                                                                                                                                                                                                                       ! P55215 rattus norvegicus (rat). caspase-2
                                                                                                                                                                                                                                                                                                                                                                                          ! P01084 triticum aestivum (wheat). alpha-am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! P01083 triticum aestivum (wheat). alpha-am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! P01085 triticum aestivum (wheat). alpha-am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P16430 escherichia coli. formate hydrogenl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P28153 rhizobium leguminosarum (biovar vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! 034483 bacillus subtilis. hpr(ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43120 mus musculus (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prote
                                                                                                                                                                                                                                                                                                                                                                                                                       μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAPQ
                                                                                                                                                                                                                                                                                                                                                                      ISIA_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPRA_SAGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPB_SALTY
                                                                                                                                                                        KDUD_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMN_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDNR_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDI_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::
                                                                                                                                                                          ck: 3484 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 9024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               len:
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x{69}(V)x(S)(P)xx(V)(S)(K)xx(P)xxx(S)x{122} 1: MKSTTFLALFLLSAIISHLPSSTADDDLVDAEGNLVENGGTYYLLPHIWAHGGGIETAKTGNE RNGNRRLVVTEENPLELVLLKAKSETASSH

203 ! P72002 mycobacterium tuberculosis.

len: 332 ! P39343 escherichia coli. l-idonate

1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)
x[10](I)x(T)(L)xx(V)(T)(K)xx(V)xxx(I)x[306]
x[10](I)x(T)(L)xx(V)xxx(I)x[306]
mnhhrisiqdiatlagyrkmtysryirspkkvaketgeriakimeeinyipnrapgmllnaqs
krvrhkilyigskddtrderokdammlhnisplrnneraissihligmolmrd
alsanpdldgyfctnddiamgallicrernlavpeqisiagfhgleigrqmipslasvitpredigrmaaqmllskiknndhnhn

ck: 6528 len: 131 ! P09182 escherichia coli. colicin n immun

ck: 6434 len: 424 ! P18642 salmonella typhimurium. dqmi prot

181

P31608

sagittaria

ck: 4153 len: 342 ! Q55274 synechocystis sp.

L

254 ! P50842 bacillus subtilis.

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q
x(143)(A)X(P)(A)X(Y)(T)(R)XX(A)XXX(A)XXX(A)XXX(C)
x(143)(A)X(P)(A)XX(Y)(T)(R)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XXX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)XX(A)X
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x(157)(L)x(P)(L)xx(P)(L)xx(A)x(257)
mdlsdiekqlokataqaelialsgelsyvllsfaklokqephlpplstraihihhglspnads
1: MDLLSDIEKQLOKATAqaelialsgelbyvllsfaklokqephlpplstraihihhglspnads
LNWITDESNEDNRYDBNFLRNELIELEKERAHFDLAVORSAQHCFEQQQLINDLL
EFAKLOKQPHLPPLSTRAIHIHHGLSPNADS
LNWITDESNEDNRYDBNFLRNELIELEKERAHFDLAVORSAQHCFEQQLINDVIFAKEEANPQFQLVNKVIRRYQDSLYLTKFFSC
SEIFTEHCQIKNQFKLCQFRQYSLAKQTALLRMWLAENQLEMPSKRQLTQLINDVIFAKEEANPQFQLVNKVIRRYQDSLYLTKFFSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q
x(196)(L)X(T)(M)XX(Y)(T)(K)XX(L)XXX(I)X(108)
MARKITALIGSGMIGGILLAHLAGLKELGDIYLEDIADGIPQGKGLDISQSSPVEGFDVNLTGASDY
DTMVPLARYSTVGGIPLIDLYTMGWYKEBLEEIIQRTROGGAEIVGLLKTGSAYY
APAASAIEMAESYLKDKKRVLPCAAHLSGQYGVKDMYVGVPTVIGAGGVERIIEIDLNKTEKEAFDKSVGAVAGLCEACINIAPALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d)
x(141)(P)x(T)(P)xx(T)(x)(F)xx(A)xxx(A)xx2(40)
x(141)(P)x(T)(P)xx(T)(F)Xx(A)xxx(A)xx2(A)x(240)
MQGISVTGLVKRGMVRSVFDTIDGIDQLEGOLASVTVTLDKLAAIQPQLVALLPDEIASQQINRE
AATFKDIQDGATYDLLIAGIAALSLILLIMMITTRSLVAALVIVGTVALSLGASFG
AATFKDIQDGATYDLLIAGIAALSLILLIMMITTRSLVAALVIVGTVALSLGASFG
LSVLVWQHLLGIQLYMIVLALAVILLLAVGSDYNLLLISREKEEIGAGLNTGIIRAMAGTGGVVTAAGLVFAATMSSFVFSDLRVLGQ
                                                                             MAUF_PARDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KR1_HSVBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MESJ_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDH_RHILV
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                                                                                                                                                                                                                                                                                    MTDA_METEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 2319 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 7474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 1419 len: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 1410 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ck: 8809 len: 236
                                                                                                                                                                                                                                                                                           ck: 9524 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 4418 len: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5295
1414
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       len:
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       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i p29897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! 033525 rhizobium leguminosarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p38371 myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Q10773 mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                   ! p55818 methylobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p44689 haemophilus influenzae. putative
       P43443
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           xenopus
               laevis
               (african
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative
                                                                                                                                                                                                                                                                                                               methyl
                       frog
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ck: 8799 len:
             229
 ! P09135 klebsiella
  nify
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ck: 7169 len: 271 Q00278 aspergillus parasiticus.

NOR1_ASPPA

NU1M_COTJA ck: 6471 len: 72 ! P24968 coturnix coturnix

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x(8){L)x(S)(I)xx(A)(T)(K)xx(L)xxx(S)x{48}
SELSPSELESITLATKVLLLSSSELWIRASYPRERYDOLMHLLMKNFLPLTLAMCLMHTS</pre>

NU5M_ANSCE ck: 1655 len: 214 ! Q31651 anser caerulescens

NU6M_APILI ck: 6545 len: 167 ! P34857 apis mellifera ligustica (common

ck: 3961 len: 263 1 P40915 neurospora nadh-ubiquinor

NUKM_BRAOL ck: 9647 len: 215 P42027 brassica oleracea

NUOJ_ECOLI <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{1,3}(L)x(T)(L)xx(I)(T)(H)xx(P)xxx(L)x{155}
MEFAFYICGLIAILATLRVITHINPVHALLYLIISLLAISGVFFSLGAYFAGALEIIVYAGAI</pre> ck: 2909 len: 184 P33605 escherichia

NUZM_NEUCR $<(x) \{1,200\} (L,I,V,M,A,P)X(P,T,S) (L,I,V,M,A,P)XX(L,I,V,M,X|106\} (L)X(S)(V)XX(A)(T)(H)XX(V)XXX(G)X(79)$ 7750 P19968 neurospora crassa.

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1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(T,Y,M,A,P)XX(L,Y,M,A,P,XX(I))(T,Y,M,A,P)XX(I)X(T,Y,M,A,P,XX(I)X(T,Y,M,A,P)XXX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I)X(T,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX(I,Y,M,A,P)XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{9}(L)xx(E)(S)(R)xx(I)xxx(I)x{302}

MSFKKFPRHLISIRDLSRGEIVKDIVASEIKQAYKQNFQNRRSVQMSGLSSQNVAMIFSKRSTRT
MIANAKVGIHTSVAKPKUVUVRDDILSIVNEAANSUNGSTFEIVNDFKVAVKNADIV
VTDTWISMGQEAEKEQRLKQFTGFQVTGEIMKLAKPSCKFMHCLPRHPEEVSDEVFYGENSLVFQEAENRKWTTVAVLEALLVNRGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(3)(L)x(S)(V)xx(L)(S)(K)xx(I)xxx(L)x(282)

1: MENLLSVKDLSKQQILDLIALAKAVKANPABEYSQALAGKSIVTIYEKPSLRTRVTFDIGIHKLGGH
CPRGSSPDAQIVKQAMALAEISGGKINVTUNLDALVDYDVIYGDTWYSMGDDTPLA
QVKEKYMPYQINKALLMRTGIKHVLHCQPAHRELEITSEVMDGEHSLIFDQAENRMHAQNAVLLTLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *(185)(1)x(5)(1)x(7)(8)xxx(4)xx(1)x(105)

MLKFILRRCLEAIPTLFILITISFFMMRLAPGSPFTGERTLPPEVMANIEAKYHLNDPIMTQYFS:
MVALSLAYIASIARITRGSMIEVLHSNFIRPARAKGLPMRIILEHALKPALLPVL
SYMGPAFVGIITGSMVIETIYGLPGIGQLFVNGALNRDYSLVLSLTILVGALTILFNAIVDVLYAVIDPKIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x[18])(L)X(P)(A)X(W)(S)(R)XX(P)XXX(L)X(176)

1: MESFAVAAAQLGPHFAPLSNGSVVDKVTDEDMHLISPYWNQFPAMDPIWAKILTAYMIMIGMISWC SIWCLAPAFGWSRYVPEGNLTSCGIDYLEEDDWNFRSYLIFYSIFVYYIPIFLICYS
YWFIIAAVSAHEKAMREQAKKMNVKSLRSSEDAEKSAEGKLAKVALVTITLWFMAWTPYLVINCMGLFKFEGLTPLNTIWGACFAKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x(179)(L)X(P)(V)XX(W)(S)(R)XX(P)XXX(L)X(176)

1:
MERYSTPLIGSSFAALINGSVTDKYTPDMAHLVHPYWNQFPAMEPKWAKFLAAYMVLIATISWCGN
WTLAPVFGWSRYVPEGNLTSCGIDYLERDWNPRSYLIFYSIFVYYLDLFLICYSYW
FIIAAVSAHEKAMREQAKKMNVKSLRSSEDADKSAEGKLAKVALVTISLMFMAWTPYTIINTLGLFKYEGLTPLNTIWGACFAKSAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1:\\ \texttt{MASKVVTGVVKTTAGGVVPVSQKYTVQSVGVWERIRRAFAIDPNRSNGVPLVPYNRNPSPGSLDPL}\\ \texttt{WDVYKYQLABEPSYSEAYPCRSFS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPS1_DROPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 4920 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 9240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ck: 7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 4358 len: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 9791 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <(X)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X\{185\}(I)X(S)(I)XX(I)(R)XX(M)XXX(L)X\{105\}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      len:
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                                                                                                                                                                                                                                                                                                             341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! P31132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P96172 vibrio sp. (strain 2693). ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! P28678 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! P06002 drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! P22269 calliphora vicina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P31317 schizosaccharomyces
                                                                                                                                                                                                                                                                                                P31228 bos taurus (bovine). d-aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               escherichia coli. oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pseudoobscura
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                                                                   PLEK_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::
                                                                                                                                                                                                                                   <a>(X) {1,200} {L, I, V, M, A, P) X (P, T, S) (L, I, V, M, A, P) X (L, I, V, M, A, F, Y, W, X, T) {A} X (T) {A} X (T) {A} X (L) {S} (H) X (L) X (L) X (L) X (B) X (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 804
                                                                   ck: 1536
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len:

350

! P08567 homo

sapiens

126

263

Q40708 oryza

sativa

! P16678

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GGTRQKGDWNLSPDAEISKEILSRCCALEPSLRGAYDLREKVGLRPTRPSVRLEKELLAQDSRRLPVVHHYGHGSGGIAMHWGTA
                                                                                                                                                                              ck: 166
                                                                                                                                                                                                             <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{68}(L)x(S)(V)xx(V)(T)(K)xx(L)xxx(L)x{82}
MADTGAPGGETLLFLTDEQLRKGIEAMFFAYRGFTADPDRILDQHDYGRAHHRAIHFINREPG</pre>
                                                                                                                                                                                                                                                           ck: 1875 len: 166 ! P31078 rhodobacter capsulatus (rhodopseu
                                                                                                                                                                                                                                                                                                                                                                   ck: 7545 len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 7167 len:
                                                                       ck: 2829
                                                                       len:
                                                                                                                                                                            len: 441
                                                                       246
                                                                                                                                                                                                                                                                                                                                                                    328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341
                                                                                                                                                                                                                                                                                                                                                                 ! Q15077 homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Q99489 homo sapiens (human).
                                                                       ! P14697 alcaligenes
                                                                                                                                                                             ! P28795 saccharomyces
                                                                                                                                                                             (baker's
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1 <\(X)\(1,200\)\(L,I,V,M,A,P)X\(P,T,S)\(L,I,V,M,A,P)XX\(L,I,V,M,A,F,Y,W)\)\(d)\(1,Y,M,A,P)X\(D)\(1,Y,M,A,P)XX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)XXX\(L)
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x{111}(L)X(S)(A)XX(L)(S)(L)XXX(P)XX(T)2}
MKKELIGEAS:IKNKTIAVAHAEDEBYIRAKEAAEHLSARFLLTGDSKKLNELTSSMQGHQVEI
TVNPKMEATVNAAALAOMYKRGQIRGCIVOGPLALDNAVSGIAAAQKKISGDVAGN
PDILLVPTIEAGNILYKSLIYFAKASVAAVITGAKAPIALTSRADSAENKLYSTALAICASEEYTH
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x(151)(P)X(S)(Y)XX(L))XX(L)XXX(Y)X{209}

MDVLAEANOTFALMILKTIGKDNSKNVEFSDMSMSCALAMVYMGAKGNTAAOMAQILSFNKSGGGG
DKENTBERLFKVSKNBEKPVOMÆKSGTFKATVIGEIFTGOLVLÞYVGKKLNMIIM
LPDETTDLRTVEKELTYEKFVEMTRLDMMDEEEVEVSLFRFKLEBSYDMESVLRNLGMTDAFELGKADFSGMSOTDLSLSKVVHKSFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 <((X)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d)
x(1149)(A)X(T)(V)XX(L))XXX(L)XXX(1)X(209)
MDDLCEMROTEALSLEKILIGEBDUSRAVTEEPMSISSALAMVEMGAKGSTAAQMSQALCLYKDGDI
KYTRGMLFKTNEEKKTVQMMFKEAKFKMGYADEVHTQVLELPYVEEELLAMVILLPD
KYTRGMLFKTVEKFKAWTNSEKLTKSKVQVFLPRLKLEESYDLEPFLRRLGMIDAFDEAKADFSGMSTEKNVPLSKVAHKCFVEV
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<(x){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W)(C)
x{87}(M)x(P)(I)xx(I)(T)(R)xx(A)xxx(I)x{145}
mdvkidgplysgkakdvlltddpeivavrerdditagdgekkdtlemkgyynsvisakifevleea</pre>
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<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,Y,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,X,M,A,F,
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x(7)(V)x(5)(I)xx(F)(S)(K)xx(I)xxx(I)xx(BS5)

MEWRGRDVISIRDFSKEDIEVVLSTAERLEKEMKEKOQLEYAKGKILATLEFEPSTRIRLSFE

AFYDVELYLISPELLAMPKHIVEELERGMXIVETTRLESPUGELDVLYVTRIOKE

REPDEQEYLKVKGSYQVNLKILENVKDSLKIMHPLPRVDEIHPEVDKTKHAIYFKQVFNGVPVRMALLALVLGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 <-(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,W,A,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,F,Y,X,X,F,Y,X,F,Y,X,X,F,Y,X,X,F,Y,X,X,F,X,X,F,X,X,F,X,X,F,X,X,F,X,X,F,X
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PYRB_PYRHO

ck: 9980 len:

308

i 058451 pyrococcus

PYRB_SALTY

ck: 2583 len: 310

P08420

salmonella

typhimur**ium.**

PYRB_SERMA

ck: 4826

305

! P19910 serratia marcescens. aspartate

PYRB_VIBS2

ck: 5096 len: 310

! P96174 vibrio sp. (strain

PYRZ_BACSU

ck: 2658

256

! P25983

bacillus subtilis. dihydroorotate

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ck: 3945
   310
   ! P00479 escherichia coli. aspartate
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PYRB_ECOLI

PYRB_MYCTU

ck: 1547 len: 319

1 P71808

mycobacterium tuberculosis.

PYRB_PYRAB

ck: 9304 len: 308

! P77918 pyrococcus abyssi. aspartate

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FKLEFGRDSSGRIRLGDEVSPDTCRLWDMETGEPLDKDIFRRGEEGVVGAYRRVAR
MILDDEDIERWNVEL
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		MINIVVLGSMNTDLVMRTKICPSGGETIHGEPDGFSTGNGGKGANOAVAVARLSNPADIKVSM
HDMI	KSANGESALVSACKVKA	HDMISYCAYLVPNEHEAAILLNQADSPATLENVDAYASKLLSFGVRKAVIITLGSQ GAYYKSANGESALVSACKVKAVDTTAAGDTFIGAFSNSIAHGQPLKDSLEFAAKCSAITVQRKGAASSIPSLLEVDGSFNLKKNT
	RBS_MUSAC	ck: 2518 len: 180 ! 024045 musa acuminata (banana). ribulose
Ľ		<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)</pre>
TGY	1:	X{b}(Y)X(S)(A)XX(F)(T)(K)XX(F)XXX(S)X(LDB) MVSSMMVSSAATETRASPAQSSMVAPETGLKSASAEPVTRKPNADLSHLPSNGGRVQCMKVWP
	REG5_DROME	ck: 7903 len: 298 ! Q94913 drosophila melanogaster (fruit fl
ц		<pre><(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) x{1311/A}x/S(I,I,XX(I,I,T),R)XX(I,XXX(A),X{151}</pre>
DKAY DLPY	1: 7GYGPQSSSELPVAAALT 7LSSWSGRRSAQQAPQDR	MTTAAKVILACCLIGAFHQISSSSA IP IWEELTRUKMSHLYSTFAQLVSVHCKSTAAVGGL DKAYGYGPQSSSELPVAAALTSEPSKRRLTGELVIRVRPDGSPVEEDKMMPLPRDE DLPYLSSWSGRRSAQQAPQDRHNQLLKAAALRLHPAERPPATPPDAEASVPPATGVRSRSEDPQA
	REHY_TORRU	ck: 4850 len: 218 ! P52574 tortula ruralis (moss). rehydrin.
Þ		$<(X)\{1,200\}\{L,I,V,M,A,P\}X(P,T,S)\{L,I,V,M,A,P\}X(L,I,V,M,A,F,Y,W,X\{160\}\{L\}X(S)\{L\}XX(A)\{S\}(K)XX(I)XXX(A)X\{42\}$
WQKG	1: EPVVISPSVSDEKAKQM	MGGGWALGDLYPDIQADSTMGHIKVRDYCKDGWTIIFSHPGDYPPVCTTELGKIAAYNPEFEK WQKGEPVVISPSVSDEKAKQMFPQGWETVNLPKALRWTFVD
	REP2_YEAST	ck: 6596 len: 296 P03872 saccharomyces cerevisiae (baker's
н	•	<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{16}(A)x(S)(V)xx(V)(C)(R)xx(I)xxx(A)x{264}
TEVN	/VTQLLTLVPPDRQAALI VHANTNEEVPSRRTRSRD	LVSVTQLLTLVPPDRQAALIGDLFIPESLKDIFNSFNELAAENRLQKKSELEGR TEVNHANINEEVPSRRIRSRDINARGAYKLQNIITEGPKAVPIKKRRVAIRVRGRKSRNISRV
	RFBB_NEIGO	ck: 5086 len: 346 P37761 neisseria gonorrhoeae. dtdp-gluco
ъ		<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{160}(P)x(S)(P)xx(A)(S)(K)xx(A)xxx(V)x{170}
AWQ# VEDH	RTYRLPSIVSNCSNNYGP IARALYQVVTEGVVGETY	AWQRTYRLPSIVSNCSNNYGPRQPERLIPININALSKE ISSAYVANIA IQNIROS VANDALI I ROMLESILII IAINAE RAVA VEDHARALYQVVTBGVVG5TYNIGGHNEKTNLEVVKTICALLEELAPEKPAGVARYEDLITFVQDRPGHDARYAVDAAKIRRDIG

Page

17

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(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(38)(L)X(S)(A)XX(A)(S)(R)XX(L)XXX(S)X(196) ANVSTSLSGADSKSYSKFITALEKALESKEKVSNIPLLPSASGASRYILMQLSNYDAKAITMAID NEVPSPAALSLENEAWSLLSKQIOLAQTNNGAFRTPVVIIDNKGORVEITNLASKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIPA_LUFCY
                                                                                                                                                                                                                                                                                                                                       RS13_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                   RR8_MARPO
                                                                                                                             RUVB_THETH
                                                 S27A_ECOLI
                                                                                                                                                                                         RS8_SYNY3
                                                                                                                                                                                                                                                                                                                                                                 ۲.
                                                                                                                                                                                                                                                                                                    1:
                                                                                                                                                                                                                                                                                                                                                                <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x(73)(1)x(T)(L)xx(I)(S)(K)xx(L)xxx(S)x(43)
MGNDTIANMITSIRNANLGKIKTVQVPATNITRNIAKILFQEGFIDNFIDNKQNIKDILILNLKYQ</pre>
                                                                                                                                                                                                                                                                                                                                                                                                     ck: 6002 len: 132
                                                                                                                                                                                                                                                                                                   <(x)(1,200)(L,I,V,M,A,F)X(P,T,S)(L,I,V,M,A,F)XX(L,I,V,M,A,F,Y,W)(
x(17)(V)x(S)(F)xx(W)(C)(K)xx(A)xxx(V)x(117)
grmHSKGKGIASSALPYVRSPPAWCKADADSVYEQILKFSKKGMSPSQIGVTLRDSHGIPQVRFT)</pre>
                                                                                                                                                                                                                                                                                                                                        ck: 3858 len: 150
                                                                                                                                                       ck: 8926 len: 133
                                                                                                                             ck: 3575
                                                   ck: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                 len:
                                                   len: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                  324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! Q00465 luffa cylindrica (smooth loofah)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P22851 luffa cylindrica (smooth loofah)
                                                                                                                                                                                                                                                                                                                                          ! P28189 schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                      ! P06362 marchantia polymorpha (liverwort).
                                                                                                                                                                                              ! P73307 synechocystis sp. (strain
                                                                                                                                 ! Q56214 thermus aquaticus (subsp.
                                                    1 P26428
                                                    escherichia coli. sigma cross-reacti
                                                                                                                                                                                                                                                                                                                                               pombe (fission
                                                                                                                                       thermophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                        SSAU_SALTY
                                                                                                                                 SSR1_HUMAN ck: 8652 len:
                                                                                                                                                                                                                                                                              SRP_CHLPS
                                                    SSR1_MOUSE
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۳.

ck: 3263 len: 352

! P96069 salmonella typhimurium.

391

i p30872 homo sapiens

(human).

ck: 8110 len: 391

1 P30873

mus

musculus

ck: 9648 len: 134

<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{34}(I)x(S)(V)xx(W)(C)(R)xx(I)xxx(I)x(84) wsgenansicsdutsliopcleovmodeguovslinsvigwcevhiinpiktskivosrafqi

! P28164 chlamydia psittaci. sulfur-rich

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SECY_RICPR
                                                                                                                                                                                                                                                                                                                                                             SIXA_ECOLI
                                                                                                                                                                                                                                                                         SIXA_HAEIN
                                                                                                                                                                                     SPAL_SALTY
                                                                                                                                                                                                                           ۲.
                                                                                                                                                                                                                                                                                                             <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 3620
                                                                                                                                                                                                                                                                                                            <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{99}(V)x(S)(V)xx(I)(S)(H)xx(L)xxx(L)x{46}
MQVFIMRHGDAALDAASDSVRPLFINGCDESRLMANWLKGQKVEIERVLVSPFLRAEQTLEEV</pre>
                                                                                                                                                                                                                                                                                                                                                                ck: 9360 len: 161
                                                                                                                                                                                                                           <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X,106)(V)xx(S)(V)xx(V)(S)(H)xx(L)xxx(I)x(42)
wnifimrhgeaevmansdkarhltvygskoaflogowlkohlstlvinsldrilvspyvraqe</pre>
                                                                                                                                                                                        ck: 7477 len: 432 ! p39444 salmonella typhimurium.
                                                                                                                                                                                                                                                                           ck: 2974 len: 164 ! P44164 haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433
                                                                                                                                                                                                                                                                                                                                                                    p76502 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Q9zcs5 rickettsia prowazekii.
                                                                                ! P21625 spiroplasma melliferum.
                                                                                                                                                                                                                                                                                                                                                                         phosphohistidin
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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(91)(P)x(F)(Y)xX(F)(T)(H)xx(F)xx(S)x(152)

MYKETVYSAFNLLMHYPPPSGAGQHPQPPPLHKANQPPHGVPQLSLYEHFNSPHPTPAPADISQK
LKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKRR
SREKHQESTTETNWPRELKDGNGQESLSMSSSSSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(148)(V)X(S)(M)XX(Y)(S)(K)XX(P)XXX(T)X{114}

1: MEEKKRLALIEKORIAEEKIASGRKIRKRISTNATKHEREFVKVINSMFVGPATFVFVDIKGNKSHAIFGFDYGKKPGRNVDIIGQGRPIITKRGSILYLTFTGFSALMGHLENFTGKHEP
VFYVRTERSSSGRSITTVVNGVTYKNLREFIHPYNFVSSKTORIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 <(x)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(188)(I)x(P)(I)x(F)(S)(R)xx(A)xxx(G)x(187)

MFPMGTAPSPTSSPSSSFGGCGEGVCSRGPGSGAADGMEEPGRNSSQNGTLSEGGGSAILISFIYS
NLGVWVLSLLVILPIVVFSRTAANSDGTVACNMLMEEPAQRWLVGFVLYTFLMGFL
LPVGAICLCYVLIIAKMRMVALKAGWQQRKRSERKITLMVMMVVMVFVICWMPFYVVQLVNVFAEQDDATVSQLSVILGYANSCANPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(1)(P)X(P)(A)XX(F)(X)X(L)XXX(C)X(258)

1: MMSDYTWFEGIPFPAFWFSKEILENSCKKFVVKEDDLIILTYPKSGTNWLIEIVCLIQTKGDPKWINFLVLYYEDMKKDTMGSIKKICDFLGKKLEPDELNLVLKYSSFQVVKENNMSNYSL
MEKELILTGFTFMRKGTTNDWKNHFTVAQAEAFDKVFQEKMAGFPPGMFPWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(43)(L)X(T)(A)XX(L)X(T)(H)XX(P)X(155)

1: MEVLETAMACLIVYIYYIYIDEEKKRELKVRNKMTNLLFEQFLLLTTASSLTHISAQTVPPPPPPPT
KKSIELGCAQRTCYEGPATLTVCFYNPPGNVIGEKPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKSKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKTKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lpvgaiclcyvliiakmrmvalkagmqorkrserkitlmvmmvvmvfvicmmpfyvvqlvnvfaeqddatvsqlsvilgyanscanpj
TELT_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T2C1_CHVI3 ck: 7233 len: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFI_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ST14_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSRB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSRB_CANFA
                                                                                                                                                                                                                                                                                                      CF1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUH3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSR1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>! '</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 4
                                                                                                                                                                                                                                                                                                      ck: 5007 len: 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ck: 800
                                    č
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 5285 len: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ck: 9240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x{82}(I)x(P)(A)xx(V)(S)(H)xx(V)xxx(L)x{85}
mrllsevvlalfavtqaeegarllasksllnryavegrdltlqynIynvgssaaldvelsddsfpf</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)
x{82}(I)x(P)(A)xx(V)(S)(H)xx(V)xxx(L)x{85}
mrllasvilalfavshaeegarilasksilnryavegrdltiqyniynvgssaaldvelsddsfer</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 8392 len: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ck: 8093 len: 183
                                    3375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  len: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               len: 391
                                    len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    len: 311
                                    167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! P52283 chlorella virus il-3a (cv-il3a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! P50235 rattus norvegicus (rat). alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P44847 haemophilus influenzae. sufi protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! P43308 homo sapiens (human).
                                                                                                                                                                                                                                                                                                      ! P36402 homo sapiens (human). t-cell-specif:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! Q41495 solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! P28646 rattus norvegicus (rat). somatostat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! P23438 canis familiaris (dog). translocon
                                 015273 homo
                                 sapiens
                                 (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (potato). sts14 pr
                                    telethonin
```

1:	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W,X)(1,1,1,V,M,A,F,Y,W,X)(1,1,1,X,P)(V)xx(V)(S)(K)xx(A)xxx(S)x(12) MATSELSCEVSEENCERREAFWAEWKDLTLSTRPBEGCSLHEEDTQRHETYHQQGQCQVLVQR</pre>
TELT_MOUSE	ck: 5613 len: 167 O70548 mus musculus (mouse). telethonin
1:	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(139)(L)x(P)(V)xx(V)(S)(K)xx(P)xxx(T)x{12} manselsconseengermaewadlilstreeegcslheedtgrhetyhrogocoanvor</pre>
TRAM_AGRT6	ck: 4597 len: 102 ! Q57471 agrobacterium tumefaciens. transc
1:	<pre><(X){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W x{13}(L)x(P)(L)XX(L)(T)(R)XX(P)XXX(L)X{73} MELEDANVTKKVELRPLIGUTRGLPPTDLETITIDAIRTHRRLVEKADELFQALPETYKTG</pre>
TRMD_SYNY3	ck: 6210 len: 231 P72828 synechocystis sp. (strain pcc 680
1 YTRPPVFRGLAVPPVLLSGNH	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W x{70}(V)x(S)(L)xx(L)(S)(K)xx(V)xxx(T)x(145) 1:</pre>
TRMU_SCHPO	ck: 7997 len: 415 ! 013947 schizosaccharomyces pombe (fissio
1 PTDKRKDQTLFLCTIRKEALE CFVSPNVGRKFRKFLQRYLNF	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(200){I)x(P)(L)xx(W)(T)(K)xx(V)xxx(A)x{199} mRYSLFLQKQIIECSKAFQPHSTRLQWFRKSQDKVFVAMSGGVDSSFSAYLLKSQGYNVEGVFM MRYSLFLQKQIIECSKAFQPHSTRLQWFRKSQDKVFVAMSGGVDSSFSAYLLKSQGYNVEGVFM KTIFPLHNWTKENVKQASSAGFKEIAEKQESQGL 'SDRPIKVIAGKNVVGEFSGNHGIWSLTVGERCGLSLPQAQSEYFGRWYVWKKDIKNNALYICRG</pre>
TRMU_YEAST	ck: 8415 len: 417 i Q12093 saccharomyces cerevisiae (baker's
1 PKDQSYYLSQINSTYLSSLLL SQHGKFKNFLKHYLPSSPGDI	<pre><(X){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W x(196}(L)x(P)(I)xx(L)(T)(K)xx(V)xxx(A)x{205} MLARYLNLIGRRSASPYRPORLPAKEDNVIVAMSSGVDSSVAAALFAGEFPNTRGVYMQNWSE ,PIGHLTKPEVRDLAKYAGLPTAEKEDSQGICFVNN .ITVDPQSGAKTTWGRHDGLWSYTIGQKVGISMPQADPNYQGTWFVSEKLRDINEILIVRGRDNP</pre>
TRNH_DATST	ck: 5293 len: 268 P50165 datura stramonium (jimsonweed) (c
1 TKSLACEWAKDSIRVNAVAPW SEVSSLYTYLCLPTASYITGQ	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W</pre>
TRPF_CRYNE	ck: 2342 len: 312 ! P27710 cryptococcus neoformans (filobasi
1: GLDLYQLHGDEPQAWAKFIPV SGGGGEGKAFPWEHAKRLIQS	<pre><(X)[1,200](L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F,Y,W x[62](L)x(P)(L)xx(V)(S)(K)xx(P)xxx(1)x[234] MSTTSRVNAALNGRDVVLCALSGISSHEDVEKYVKEGVKGVLVGEALMRASDTKAFLRSLIGL IPVPVVKVFRVSPEGIVRGGEIRRPGLNQAILLDAGGA IQSGEVGSEGHVPLPVILAGGLTPENVGQALNRLVKAFGVWMSAVGSKEREGRSRRRLRRS</pre>
TTF1_CANFA	ck: 4988 len: 371 ! P43698 canis familiaris (dog). thyroid t
1: RRFKQQKYLSAPEREHLASMI	1

VEZ_HPV28 ck: 1816 len: 376 P50771 human papillomavirus type 28. reg <pre></pre>	TTFI_RAT Ck: 6608 len: 372 P23441 ratus porregious (rat). Thyroid tratically care to porregious (rat). Thyroid tratically care to porregious (rat). Thyroid tratically care to provide tratically care tra
VEZ_HPV18 ck: 5006 len: 365 ! p06790 human papillomavirus type 18. reg <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W *(61)(V)X(P)(A)XX(I)X(1)X(1)X(1)X(1)X(2)X(2)X(2)X(2)X(3)XXX(1)X(1)X(2)X(2)X(2)X(2)X(2)X(2)X(2)X(2)X(2)X(2	INDS INDOCESSOR (S.T., V.M., A.F., Y.W. XX(A), XXX(S), X(214) EGGGLGAPLAAYRQGQAAPPAAAMQQHAVGHHGA EGGGLGAPLAAYRQGQAAPAAAAISVGSGGAGLGAHE SHAQQQAQQAQAAQAAAAISVGSGGAGLGAHE
VE2_HPV10 ck: 273 len: 376 ! P36781 human papillomavirus type 10. reg <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{57}(V)x(P)(P)xx(V)(T)(K)xx(A)xxx(I)x{303} METLANRLDACODKWLELYROSOKLEDQITHWHLELYKARECGLTHIGHQVVPPLS CVYGETGKWEVHVGGKVIHHDAFDPVSSTREISTPGPVCTSNTTPASTQAVGASE GPEQKRQRLEAVDGQHQQQRQGSKDSTQKAAERAGGQVDSDRTRLCDTRSAHPVRHPSDPDCAPVIHLRGDPNSLKCFRYRLHHG	ck: 5439 len: 371 ! P43699 <(X)[1,200](L,I,V,M,A,P)X(P,T,

<(X)[1,2		н	1: MSQGSRPTSSDIAVNQRECYKVEGFKVVSTRLRSAEYESFSHQARLLGLSDSMAIRVAVRRIGGFL	
ck: 7061	VRPR_SALDU		<(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,Y,	1
MLLPVVAR	1:		VID1_AGRT5 ck: 2312 len: 147 ! P18591 agrobacterium tumefaciens. t-dna box	
ck: 6252 <(X){1,2 x(18)(VP8_вррн6	μ .	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C</pre>	ь
MPLTPP	1.		VID1_AGRRA ck: 2761 len: 147 ! P13461 agrobacterium rhizogenes. t-dna bord	
ck: 3415 <(X){1,2 x(2)(L	VMEM_PVMR	н	x{22}{A}x(\$)(A)xx(L)(\$)(X)xx(A)xxx(A)x{12} MLVARESLAEHYKEVEAFQTARAKSARRLSKIIAAVAAIAILGNVAQAFAIATMVPLSRLVPVYLK GKMPVVSTWTATVRYEKVTSLPGRLRLTNPAGLVVTSYQTSEDTVSNVGQGAP	GKMPVV
,			<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C	۲
<(X){1,2 x{2}(L MPLTPP	1.		VIB8_AGRT9 ck: 2826 len: 230 P05357 agrobacterium tumefaciens. virb8 pro	
ck: 8138	VMEM_LVX		(X) (1,200) (L,1,V,M,A,E)X(F,T,S)(L,1,V,M,A,E)X(F,T,Y,M,A,E,Y,M)(C)	GKNBVI
<(X){1,2 x{22}(MPLTPP	:	Þ	VIB8_AGRT6 ck: 2646 len: 230 P09781 agrobacterium tumefaciens. virb8 pro	
ck: 566	VMEM_CVB		EP	HSEP
MSRRNPCK	1:	DIGVNEQNE	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C X{29}(A)x(S)(A)xx(L)(S)(K)xx(A)xxx(T)x{192} MKGSEYALLVAREFLAEHYKEVEAFQTARAKSARRLSKVIAAVATIAVLGNVAQAFTIATMVELIF	1
<(X){1,2		ш	VIB8_AGRT5 ck: 5994 len: 237 ! P17798 agrobacterium tumefaciens. virb8 pro	
ck: 6559	VMA2_ORSVW		ILVSDTVLASINLYFVLTTFWYMMTEMFLQDYLKLQFGFYLGVFSGSLILLLPVLRYEAVFVSANLHKTVAVNIAMIPAMCVIAMM	FYILVS
x{83}(x{83}(MSRRNPCK	1: HAKNNDTT	1: ESTVSDTNDHAKNNDTT	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C)	1 SPKWSV
ck: 9828	VMA2_HRSVA		VGLM_HSVSA ck: 7071 len: 366 ! Q01017 herpesvirus saimiri (strain 11). gly	
<(X){1,2 x{83}(MSRRNPCK	1 :	1 DINVDEQNE	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{150}(V)X(S)(A)XX(A)(S)(R)XX(L)XX(L)X(206) 1: MGGRSLOGLALICLIMVGATGLIVVRGPTYGLUSDSLUDAGAVGPQGFVEEDLRVFGELHFVGAQVPH DYGSCDPAQLPFSAPRLGPSSVYTPGASSRPTPPRTTTPPSSPRDPTPAPGDTGTPA PASGETAPPNSTRSASESRHRLTVAQVIQIAIPASTIAFVFLGSCICFIHRCQRRYRRPRGQIYNPGGVSCAVNEAAMARLGAELRSH	1 DYGSCI PASGEI
ck: 6337	VMA2_BRSVA		VGLI_HSV2H ck: 501 len: 372 ! P13291 herpes simplex virus (type 2 / strai	
<(X){1,2 x{102} MDGLGVRN IVFCIMLGT PLELAREIY	1 (X)[1,2 x(102) 1: x[102] DSKIKLMNSDYVHDRGLIRGAIVFCIMLGT DTIGLKRKRSRKNTLNNIKTKPLELAREIY	1 DSKIKLMNSI DTIGLKRKR	<pre><(X)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F) x(29)(V)x(S)(V)xx(L)(S)(R)xx(I)xxx(A)x(132) MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHV)</pre>	.
ck: 889	VLF1_NPVOP		VGG_BPG4 ck: 4484 len: 177 P03644 bacteriophage g4. major spike protei	
	1:	.	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{100}(V)X(P)(L)X(L)(S)(K)XX(L)XX(L)XX(L)XX(201) WITITKERIELFYKSPLENGLTREGOMELARIALASLDAETVRYLNKFSGTCVTLEQQPNAADDVAESVVPEECPAELPYAQVKAVADLYALCWQSGSVVTYTPDEEXATIWINNSGTCVQ EYVKLERLQEALAGNSPVIPGGWISCSERWPDNDESKPIAIFTGKCLGQGMFVATYDDDGFFDYWEGMEIIGVSHWMQLPDPPL	1 ESVVPE
Ck: 4145	VIDI AGRTA		VEAA_BPP22 ck: 7758 len: 317 ! Q03544 bacteriophage p22. eaa protein. 10/1	

	VID1_AGRT6	VID1_AGRT6 ck: 4145 len: 147 '! P06667 agrobacterium tumefaciens. t-dna
H		<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) x{125}(L)x(S)(I)xx(V)(S)(R)xx(I)xxx(S)x{6}</pre>
		MSKHTRVTSSETALNQHRSLNVEGFKVVSARLRSAEYETFSYQARLLGLSDSMAIRVAVRRIG
	VLF1_NPVOP ck: 889	ck: 889 len: 374 ! O10330 orgyia pseudotsugata multicapsid
μ .		<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)</pre> <pre>x(102)(L)x(S)(P)xx(L)(C)(K)xx(L)xxx(S)x(256)</pre>
DSKIKLMNS DTIGLKRKR	1: DYVHDRGLIRGA SRKNTLNNIKTK	MDGLGVRNETTFNDWKARIQSASRFEHVFDLATDRQRCTPDEVKNDSLWSKYMFPKPFAPTTL DSKIKLMNSDYVHDRGLIRGAIVFCIMLGTGMRINEARQLSVDDLNVLIKKGKLRS DTIGLKRKRSRKNTLNNIKTKPLELAREIYARNPTVLQISKNTSTPFKDFRRLLDEAGVEMERPRSNMIRHYLSSNLYNSGVPLQ
	VMA2_BRSVA	VMA2_BRSVA ck: 6337 len: 186 P29792 bovine respiratory syncytial viru
-		<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W

1 DINVDEQNE	_
: .	VMA2 BRSVA
<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{83}(L)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x{87} MSRRNPCKYEIRGHCLNGKKCHESHNYFEMPPHALLVRQNFMLNKILKSMDRNNDTLSEISGA</pre>	VMA2 BRSVA ck: 6337 len: 186 ! P29792 bovine respiratory syncytial viru

VMA2_HRSVA ck: 9828 len: 194 ! P04545 human respiratory syncytial virus (X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) x(83)(I)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x(95) MSRRNPCKPEIRGHCLNGKRCHFSHNYFEWPPHALLVRQNFMLNRILKSMDKSIDTLSEISGA	1		ь		
<pre>ck: 9828 len: 194 ! P04545 human respiratory syncytial virus <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x{83}(I)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x{95} MSRRNPCKFEIRGHCLNGKRCHFSHNYFEWPPHALLVRQNFMLNRILKSMDKSIDTLSEISGA</pre>		1:		VMA2_HRSVA	
		x{83}(I)x(S)(I)xx(I)(T)(K)xx(A)xxx(M)x{95}	<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	ck: 9828 len: 194 P04545 human respiratory syncytial virus	

ESTVSDTNDHAKNNDTT	1.	1-3
	X(83)(1)X(S)(1)XX(1)(T)(K)XX(A)XXX(M)X(95) MSRRNPCKFEIRGHCLNGKRCHFSHNYFEWPPHALLVRQNFMLNRILKSMDKSIDTLSEISGA	<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W

VMA2_ORSVW ck: 6559 len: 186 ! Q84132 ovine respiratory syncytial virus			3	I T V M	{1.200}(I.T.V.M.A.D)X/D.T.S)/I.T.V.M.A.D)X/I.T.V.M.A.E.V.I		
	ratory s	ovine respi	! Q84132	len: 186	ck: 6559]	VMA2_ORSVW	
							į

		IGVNEQNE
x{83}(L)x(S)(V)xx(I)(T)(K)xx(A)xxx(M)x{87} MSRRNPCKYEIRGHCLNGKKCHFSHNYFEWPPHALLVRQNFMLNKILKSMDRSNDTLSEIS	1.	
<(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,F,Y,F,Y,F,Y,F,Y,F,Y,F,Y,F,Y,F,Y,F		

VMEM_C	YB ck: 560	len:	106 !	P37989	VMEM_CVB ck: 566 len: 106 ! P37989 chrysanthemum virus b (cvb). 11.	virus b	(cvb).	11.4
	<(x){1,	200)(L, I	, V, M, A, F)X(P,T,	<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,I))XX(L,I,	V,M,A,F	1' X'.
1	MPLTI	PPDHTKVLI	LVAAIGLS	IVASILT	MPLTPPPDHTKVLLVAAIGLSIVASILTYSRNTLPQVGDHSHLLPHGGVYKDGTKTIVYG	LLPHGGVY	KDGTKTI	YYG O

	1:
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<u>}</u>	¥.
0130	LTPPP
200	DHTKVL
108	LVAAIC
-	37.5
107001	IVASIL
1 : 1 :	TYSRNI
3	LÞQVGI
;	SHC
TIP 6. 0130 100 100 1073331 1:1:	MPLTPPPDHTKVLLVAAIGLSIVASILTYSRNTLPQVGDHSHLLPHGGVYKDGTKT
	PKT.

1.		VMEM_LVX
<pre>MPLTEPPDYTKPFIAVVVGGTLAAFVLLLTRNTLPHTGDNLHSLPHGGTYCDGTKRIRYGG</pre>	<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	VMEM_LVX ck: 8138 len: 108 ! P27331 lily virus x. hypothetical 11.8 k

	VMEM_PVMR	
<(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)	VMEM_PVMR ck: 3415 len: 109 ! P17527 potato virus m (strain russian) (
(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W	otato virus m (strain russian) (

<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(18}(A)x(T)(P)xx(V)(S)(R)xx(A)xxx(S)x(115} MLLPVVARAAVPAIESAIAATPGLVSRIAAAIGSKVSPSAILAAVKSNPVVAGLTLAQIGSTG</pre>	1: .	
VP8_BPPH6 ck: 6252 len: 149 ! P07579 bacteriophage phi-6. major nucleo	VP8_вррн6 с	
<pre>x(3)(1)(0)(0)(0)(0)(0)(0)(0)(0)(0)(0)(0)(0)(0)</pre>	1:	

	VRPR_SALD	
<(x)	U ck:	
[1,200	7061	
)}(L,I	len:	
, v , m ,	297	
A,		
)X(P,T	P24417	
$<(x)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,E,E,E,E,E,E,E,E,E,E,E,E,E,E,E,E,E,E$	VRPR_SALDU ck: 7061 len: 297 ! P24417 salmonella dublin. virulence ger	
, A, P) XX (dublin.	
L, I, V, M, A, E	virulence	
, Y ,	gen	

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1 

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                                                                                                                                                                                                                                                                                                                                                                                                                            1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q

x(115)(A)X(S)(A)XX(I)(S)(H)XX(A)XXX(T)X(223)

MRARPQYCEALLFALALOTGYCYGIKWLAEKTPSALALNOTOHCKOLEGIVSAQVOLCRSNLELM

VKKTGSQANKLMRLHNSEYGRQALASLEKKEKCHGVSGSCSIRTCWKGLOELQDY

AADLKTRYLSATKYVHRPMGTRKHLVPKDLDIRPVKDWELVYLQSSPDFCMKNEKYGSHGTODROCNKTSNGSDSCDLMCCGRGYNPY

AADLKTRYLSATKVVHRPMGTRKHLVPKDLDIRPVKDWELVYLQSSPDFCMKNEKYGSHGTODROCNKTSNGSDSCDLMCCGRGYNPY
                                                                                                                                                                                                                                        1 

<
                                                                                                                                               (x)\{1,200\}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d,X,\{119\}(L)X(T)(V)XX(M)(S)(H)XX(A)XXX(S)X\{18\}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! P49339
                                                                                                                                                                                                                                                                                                          ! P48615 mus musculus (mouse). wnt-11
                                                                                                                                                                                                                                                                                                                                                                                                    1 096014 homo sapiens (human). wnt-11 protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P51891 coturnix coturnix japonica (japanes
                                                                                                                                                                                                                  ! P40589 drosophila melanogaster
                                                                                                                         i 010280 orgyia pseudotsugata
                                Q15053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gallus
                                  homo
                                sapiens (human). hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gallus (chicken).
                                                                                                                             multicapsid po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wnt-11
                                                                                                                                                                                                                                                                                                                 protei
                                                                                                                                                                                                                       fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y280_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y209_MYCPN
                                                                                                                                                                                                                                                                                                                                                  Y425_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                            7373_TREPA
                                                                                                                                                                                                                                                       Y464_MYCGE
                                                                                                                                                                Y464_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ck: 9511 len: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ck: 6533 len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                             ck: 4876 len: 477
                                                                                                                                                                                                                                                                                                                                                     ck: 2944 len:
                                                                                                                                                                                                                                                          ck: 2836 len: 385
                                                                                                                                                                  ck: 5866
                                                                                                                                                                                                                                                                                                                                                       450
                                                                                                                                                                    385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 P75485 mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! P47522 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ! 083388 treponema
                                                                                                                                                                                                                                                                                                                                                        i p75172 mycoplasma
                                                                                                                                                                                                                                                             p47702 mycoplasma
                                                                                                                                                                      p75112 mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genitalium.
                                                                                                                                                                                                                                                                                                                                                         pneumoniae.
                                                                                                                                                                    pneumoniae. hypothetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetic
                                                                                                                                                                                                                                                                hypothetic
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x(23)(A)x(S)(V)xx(I)(T)(R)xxx(I)x(258)

MDFLINKKLKIFITIMETGSFSIATSVLYITETPLSRVISGLERELKQRLFIRKNGTLIPTEFAQT
GKPDINRLAGTPVLFHEGAKNFNLDTIYHEFEQTLGITNPAFSFDNVDLFSSTYRL
QQGLAMLLIPVRVCRALGLSTDHALHIKGVALCTSLYYPTKKRETPDYRKAIKLIQQELKQSTF
VRPR_SALTY
         ck: 7032 len:
            297
               ! P13041 salmonella typhimurium.
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Y209_MYCGE

ck:

308

P47451

mycoplasma

MHYVHVHRVTTQPRNKPQTKCPSGGQSQGPRGQFLDTVLAAMCPIAMLLTADPGMPPTCLWHT

WN11_CHICK

ck: 4630 len: 354

WN11_COTJA

ck: 4030

len:

354

WN11_HUMAN

ck: 3073 len: 354

WN11_MOUSE

ck: 1689 len: 354

WNT4_DROME

ck: 8394 len:

389

Y021_NPVOP

ck: 562

len:

298

Y040_HUMAN

4815

153

, P	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Qx(B)(P)X(T)(L)XX(M)(S)(K)XX(I)XXX(V)X[192] 1: MKVSVPGMPYLLNMSKNDIYKMVSGDKMDVKMNIFQRLWETLRHLFWSDKQTEAYKLLFNFVNNQSDLYERPGWNANLGVLPRTVLTRTVLTWTVLP
DPLACIEDPF ISSDEASEKY	YABP_ECOLI ck: 98 len: 216 ! P39220 escherichia coli. hypothetical 24.8
н	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x{98}(P)x(S)(A)xx(A))(S)(R)xx(A)xxx(I)x{8} 1: MALASPACSRCCAASSARMPATACCPPTGASRTCARRSIPWIAWRWITCSTATVACARSRRHWP
	YA32_PSEAE ck: 6657 len: 122 ! P21485 pseudomonas aeruginosa. hypothetical
ь	<pre>1</pre>
АХИІН	1988_METJA ck: 9981 len: 329 ! Q58395 methanococcus jannaschii. hypothetic
1	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,X,W)(Q x{100}(I)x(T)(L)XX(I)(S)(H)XX(V)XXX(V)X{166} 1: MHYGLIVETSDRGITPAAAARLAESHGFETFYVPEHTHIPVKRQAAHPTTGDASLPDDRYMRTLDF IPVLVGAAGTEKNFKWIARSADGWITTPRBVDLDEPVKLLQDLWAAAGBGLEQIV ALDVKPVPDKLARWAELGVTEVLFGMPDRSADDAAAYVERLAAKLACCV
VIMLSLALSI	Y953_MYCTU ck: 883 len: 282 P71557 mycobacterium tuberculosis. hypothet
н	1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(d x{19}(I)x(S)(I)xx(I)(T)(K)xx(L)xxx(L)x(135} mkginpfyfyigmalilasivsillitksillfillafgslvgitlityisrkilkidkgrlkke
YEIIGVTID	Y79B_METJA ck: 2865 len: 170 ! P81233 methanococcus jannaschii. hypothetic
110 5617170	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(L,I,V,M,A,F,Y,W)(C,X)(L)X(260) 1: MHFLDENIQIKIDKFYKNLDYNTKINTSEFSKEFA NFLSLNNIGFFVDSTNAQNLYLNRKYRNNLLPALKKVFKGYEKCLKRISEFSKEFA DYFGKDEFFPVEKGKYYYSFDLKTFLDFPKYLVFRLIFKILNSEGIAAKVSYKALNEAFKVEINRKKNNVLLKTNDFFLEKRHNKINI DYFGKDEFFPVEKGKYYYSFDLKTFLDFPKYLVFRLIFKILNSEGIAAKVSYKALNEAFKVEINRKKNNVLLKTNDFFLEKRHNKINI
GFDQFCKLAC	Y788_BORBU ck: 1619 len: 440 ! O51728 borrelia burgdorferi (lyme disease s
1	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x{84}(I)x(S)(I)xx(Y)(S)(H)xx(I)xxx(L)x(2} nvgnmnirdkiksiknwineikpiitivgivisavaftisilmgmlflilflilitesktirki
	Y70A_METJA ck: 4119 len: 102 ! P81311 methanococcus jannaschii. hypothetic
1 RLAISMGIKT IADYKAAQKI	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(Q x(150)(A)X(S)(A)XX(A)(T)XX(I)XX(I)XX(230) xx(I)XXX(I)XX(I)XXX(I)XXX(I)XXX(I)XXX(I)XX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XXX(I)XX(
	Y503_METJA ck: 6767 len: 406 ! Q57926 methanococcus jannaschii. putative 2
1 1	1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F,Y,W)(C)
	Y4TG_RHISN ck: 6923 len: 231 P55661 rhizobium sp. (strain ngr234). proba

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1:
ISEFSLV
                                                                                                                                                                                                                                                                                                                                                                                   YBFT_BACSU
                                                                                                                                                                                                                                                                                                                                    YCBQ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YC21_METJA ck: 2920 len: 299 ! Q58618 methanococcus jannaschii. hypothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCO8_KLEPN ck: 4280 len: 373 ! Q48454 klebsiella pneumoniae. hypothetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YBCC_RHOCA ck: 2127 len: 192 ! P26166 rhodobacter capsulatus (rhodopseu
                                                                                                YCJI_ECOLI
                                                                                                                                                                                                            ACCZ_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YC38_PORPU ck: 4681 len: 291 ! P51321 porphyra purpurea. hypothetical 3
                                                                                                                                               ۲.
                                                                                                                                                                                                                                                                          ..
                                                                                                 ck: 6021 len: 262 ! P51983 escherichia coli. hypothetical 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ck: 3388 len: 249
                                                                                                                                                                                                                                                                        ck: 3224 len: 182 ! P75855 escherichia coli. hypothetical fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{142}(V)x(T)(L)xx(L)(T)(K)xx(M)xxx(I)x{34}
MDLLFDEFRAAHVPVEEMATHYIPEAARQIGAAWDSDRIGFAQVTIAISRLQELLHALQTLVT</pre>
                                                                                                                                             <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W
x{7}(L)x(S)(A)xx(I)(T)(R)xx(A)xxx(L)x{55}
MHQNSVTLDSAGAITRYFAKANLHTQQETLGEIVTEILKDGRNLSRKSLCAKLLCRLEHAT</pre>
                                                                                                                                                                                                            ck: 1943 len: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ! 031458 bacillus subtilis. hypothetical 2
                                                                                                                                                                                                            ! P75991 escherichia coli. hypothetical 8.
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YCJZ_ECOLI

ck: 51

len: 299

! P77333 escherichia coli. hypothetical tr

x(167)(L)	1: VVSRILGRSTAQRGGYSAV	<pre><(X)(1,200)(L,T,V,M,A,P)X(P,T, <(X)(1)(P)X(P)(V)XX(A)(T)(R)XX MAKVTRDDVARLAGTSTAVVSYVINNGE</pre>
ck: 8234 len	YJR8_YEAST	o ck: 9954 len: 66 ! 005954 streptomyces coelicolor. hypothetic:
EALGPYMSQHTGIDQIGRREGAIGVETAGKLTRSSVYHQAVVLALSPEHNAIYR	1:	<pre><(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(34}(I)x(S)(L)xx(Y)(C)(R)xx(L)xxx(S)x{57} maaqnpladIqvykrykakrrmegqkknsctiayidslqyycrrslshkscfpfpsqhafsrpi</pre>
DO) {L,I,V,M,A,P)X(P,T,S) (L,I,V,M,A,P)XX(L,I,V) V)x(T)(A)xx(L)(T)(R)xx(V)xxx(A)x(14)	1 YUX_ENT	r ck: 6897 len: 107 ! p53138 saccharomyces cerevisiae (baker's ye
MLIMHQVVCATINE	1:	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(43)(I)x(P)(V)xx(A)(T)(K)xx(M)xxx(P)x(89) xMQQMVLKIGGVVVDPQEVKVESKYTGELEVTRKKVVHRMLDIIIPVGLATKLTMALSPGALAAAG</pre>
Ck: 3873 len: 1/3 P39411 eschetiche con: "IF" Ck: 1873 Len: 1/4 P39411 eschetiche con: "IF" Ck: 1874 Ck: 1874	YJJX_ECOLI	l ck: 7782 len: 148 ! P31653 bacterlophage sp01. hypothetical 16.
KVVVCDRPAPRLIELAQIAQLVVVGSHGRGGFPGMHLGSVSRAVVNSGQAPVIVARIPQDPAVPA	GSPTSGLAAEIAFDEASRI MLARRLSGWQDRYPDVVVI	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x{7}(A)x(S)(P)xx(W)(S)(R)xx(A)xxx(M)x{125} MPLSGEYAPSPLDWSREQADTYMKSGGTEGTQLQGKPVILLTTVGAKTGKLRKTPLMRVEHDGQYA</pre>
-(X){1,200}(L,1,7,M,A,P)X(P,11,3)(L,1,7,M,F)(P) x(111)(Y,X(T)(L),X(L)(S)(R),XX(A),XXX(L)X(10) x(111)(Y,X(T)(L),X(L)(S)(R),XX(A),XXX(L)X(10) x(1011)(Y,X(T)(S)(R),X(T)(R),X(L)(R)(R)(R)(R)(R)(R)(R)(R)(R)(R)(R)(R)(R)	1:	ck: 497 len: 148 Q10772 mycobacterium tuberculosis. hypothet
U ck: 1836 len: 317 ! Q10862 mycobacterium tuberculosis. hypot	YJ96_MYCTU	<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x{49}(L)x(P)(P)xx(F)(T)(K)xx(M)xxx(S)x{63} MEELICTYPYHSNLFMFLFLFFCPSKRARRGHPKFLFTLCYKSNHLIPKLLPPSLFTKRVMLNPSS</pre>
<pre><(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XA(L,I,V,M,A,E)XX(I)X(P) x(49)(Y)x(P)(P)xx(I)(T)(H)xx(I)xxx(I)x(9) MGEVRVVGIRVEQPQNQPYLLLREANGDRYLPIWIGQSEAAAIALEQQGVEPPRPLTHDLIRD</pre>	1	ck: 5798 len: 128 P40057 saccharomyces cerevisiae (baker's ye
ck: 7074 len:	у129_мусти	WNSNEIENFIYLNNTLLSEVPEPNSYFYPRKESNSKLPHYSULLEFFSSK-SLISSKY FILDVER SLYPNNMPHYPDEVTAKSAFKDDFYVPRETROHGIS TAAVWYNNOHYBOHGKISKERYOPPIEFRTVRLEKTRNAIGVPNKKYMIEGKCHQCNKWIROQGRKDVS
x{120}(L) MNEIISAAVLI	1: ILVMMATQMFLDGIRMWMKG	o
<(x){1,200}(L,	⊢	- Alicaion d
ck: 1678 len: 197 ! P46851 escherichia coli. hypothetical 21	YHGN_ECOLI	<pre><(X) 1,200 (L,1,v,m,r,f)(f,1,0)(v,m,f)(f,1) x(97)(L)x(5)(L)xx(F)(6)(R)xx(A)xx(F)x(61) xTSQLEKEAREWIEETLHTKLNAQLDLLDQLQSGVILCRICKEALGANIRYKESNMPFVQMENISA</pre>
MANNTWKLIATTÄLLSVESTULAKSY WALLALSVESTULAKSY WALLALSVESTULAKSY ISSMOVATKKSDTTRVSINDISMTEEDE ISSKOVEKKIR RRDDILSPIDCEHRAINAVRDEALRHLPELGTMPGIFGLSIATWILTKVSGY PMKENEVKNRLKEY	1: MANNTWKLIATTALLI NLESKYDLLEYAHHNKIDVISSMGVAIKSDPTRVSINI KRGIATGISVVFSNEMLDPRRDDILSPIDCEHRAINA	ck: 8869 len: 174 ! Ol4185 schizosaccharomyces pombe (fission y
(M) XX(A) (T) (K) X	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	x(1)[1,20](1,1) (1)(1)(1)(1)(1)x(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(1)(
	E E	ck: 6054 len: 131 P87132 schizosaccharomyces pombe (fission Y $(x,y) = (x,y) = (x,y$
<pre><(X) {1,200} {L,1,V,M,A,P}X(P,T,S) {L,1,V,M,A,F}X(V,Y,A,F,F,F,F,F,F,F,F,F,F,F,F,F,F,F,F,F,F</pre>	1 LRTKKGTINPPIGRORSHPT	MKTILISDEDETITRVDTICTIAKLPYLNERKKERGHFTKTIMGIHAAN ING LAGGE LEGGG TGSDKYKILGEILDKIDSGCNKEGNSCSYWYIGDS PNPSKFIKITEKIIGIPKDKISSFEADNGPAWLQFCEKEGGKGAYLVKSWDSLKDLIMQVTKM
ck: 1929 len: 302 ! p54604 bacillus subtilis. hypothetical 3	YHCT_BACSU	<pre>(x)(1,200)(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C,X)(1,200)(L,I,V,M,A,F,Y,W)(C,X)(1,X)(208)</pre>
LAAEFAPGSALKVEPVTPQVTRKGSTRMTGRDPTIVFRWQGWYGHHQHPGCSCGYGVEEKOFKP	TIGWCVKVADI LKLLCWVGX AILGLAEKDPLARIGGRLNP	ck: 1969 len: 317 : P25616 saccharomyces cerevisiae (baker's ye
1 <(X)[1,200](L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W x(62](L)x(T)(P)xx(V)(C)(K)xx(V)xxx(L)x{241}	1:	x(188)(V)x(S)(P)xx(F)(S)(R)xx(V)xxx(V)x(112) MKREIADLMAFVVVAEERSFTRAARLSMAGSALSQIVRRIEERLGLRLLTRTTRSVVPTEAGEH TSGTANRWRLIRGGREVEVRMEGQLLLNTIDLIID EKKLIRVLDKFTPDLPGYHLYYPHRRHAGSAFSLFIDRLKYKGAV
ck: 3269 len: 319 p10941 cryphonectria parasitica (chesnut	YHA1_CRYPA	

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YG29_BPSP1

YGK9_YEAST

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YF58_MYCTU

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YGLR_STRCO

1:

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1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,)}

x{93}(L)x(S)(V)xx(I)(T)(K)xx(I)xxx(I)x(208}

mkTIIISDEDETITRVDICTIAKIPYLLDRRLKPEMGHFTKTYMDGYHKYKYNGTRSLPI
LKKVSDKCSQSYNGEFDCRLLTGSDKYKILGEILDKIDSGCNKEGNSCSYWYIGDS
LKKVSDKCSQSYNGEFDCRLLTGSDKKITEKIIGIPKDKISSFEADNGPAWLQFCEKEGGKGAYLVKSWDSLKDLIMQVTN
ETDLLSILHPSINGYLLINPQENPSKPIKITEKIIGIPKDKISSFEADNGPAWLQFCEKEGGKGAYLVKSWDSLKDLIMQVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x{168}(V)x(S)(P)xx(F)(S)(R)xx(V)xxx(V)x{115}
MKREEIADLMAFVVVAEERSFTRAAARLSMAQSALSQIVRRIEERLGLRLLTRTTRSVVPT
RSVPTSVSQLIDHQAINLYLPTSGTANRWRLIRGGREVRVRMEQULLNTIDLIID
AAIDGHGLAYLPYDQVERAIKEKKLIRVLDKFTPDLPGYHLYYPHRRHAGSAFSLFIDRLKYKGAV
                                                                                                                                                                                                                       1 <(x){1,200}(L,1,V,M,A,P)X(P,T,S)(L,1,V,M,A,P)XX(L,1,V,M,A,F)XX(L,1,V,M,A,F)XX(L)XXX(G)X{282}
x(464)P)x(S)(A)xx(L)(S)(K)xXX(G)X(282)
MNSNEIENEIYLUNTILSEVPENSVETPEKCENSKLPHQSDLEEPSSACSLSKNTIID
VLENHITSREPHEYTKLPDVSLVPNUNEPHYDEDTAKSAPKDDEYVPRETRGHGIS
KLGLCPICSHQGEFIWLRTKTSAYWYHMNEVHGIHSKGRPYQPPIEFRTVRLRKTRNAIGVPNKKYMIEGKCHQCNKWIRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCQ5_YEAST ck: 1969 len: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDM1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDSA_SCHPO
                                                                                                                             YER4_YEAST ck: 5798 len: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                          YDTG_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ck: 8869 len: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,
x{15}(L)x(T)(L)xx(I)(T)(K)xx(L)xxx(5)x{100}
ppsaravkdrmeseqletlekitkyilkilsktvlevevnievihhekakhliiemidyi</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ck: 6054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <(x){1,200}{L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)X(L,I,V,M,A,F)
x{97}{L)x(S)(I)xx(F)(S)(R)xx(A)xxx(P)x{61}
mTSQLEKEAREWIEETLHTKLNAQLDLLDQLQSGVILCRICKEALGANIRYKESNMPFVQ</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                          ck: 3748 len: 344
<(X){1,200}{L,I,V,M,A,P}X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F)
x{49}(L)x(P)(P)xx(F)(T)(K)xx(M)xxx(S)x{63}
MEELICTYPYHSNLFMFLFLFFCPSKRARRGHPKFLFTLCYKSNHLIPKLLPPSLFTKR</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   len: 131
                                                                                                                                        ! P40057 saccharomyces cerevisiaė (bak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! P25616 saccharomyces cerevisiae (bake
                                                                                                                                                                                                                                                                                                                                                                                                                                              o14220 schizosaccharomyces pombe (fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ! P87132 schizosaccharomyces pombe (fis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! O14185 schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pombe (fis
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<(X){1,200}(L,I,V x{169}(L)x(S)(A MKQLKPNSKYLLYGQAL	1:	<pre>rpDC_ECOLI ck: 4986 len: 285</pre>
J ck: 3644 len: 39	YWFF_BACSU	ESTND
<(X){1,200}(L,I,V x{92}(V)x(T)(P) MVRETRVRVARVYED	1:	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(150)(V)x(S)(A)xx(A)(S)(K)xx(V)xxx(T)x(T2) . MOSIOHKTALITIGGGEGIGRATALALAKEGYNIGLIGRTSANVEKVAEEVKALGVKAAFAAADVKU IRVSALTPSTVASDMSIELNLTDGNPEKVMQPEDLAEYMVAQLKLDPRIFIKTAGL
J ck: 3649 len: 11	YU73_MYCTU	YOXD_BACSU ck: 2171 len: 238 ! P14802 bacillus subtilis. hypothetical oxid
<(X){1,200}(L,I,V x{4}(A)x(T)(P)x MTVKAMTPKEVTKKS	1:	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Q x(88}(A)x(T)(Y)xx(M)(S)(H)xx(A)xxx(A)x(57) 1: MSRPLGFIGYEFGDDEMFVQQMIEKKSNAEQAKMLEQQKKMLECTETMPEESEPVPMKCLDFEEAF
J ck: 1724 len: 36	YRKG_BACSU	YOTC_CAEEL ck: 9212 len: 161 ! Q10120 caenorhabditis elegans. hypothetical
<(X){1,200}(L,1,V x{15}(V)x(T)(A) 1: MNLIQLKKWFTILTFVL LNKQGIDTLITKMQQSASQPIIFNQ	1 1: MLEDTIKNWVGILNKQGIDT	<pre>1</pre>
v ck: 1216 len: 21	YRBC_HAEIN	YORL_TTV1 ck: 9154 len: 232 ! P19296 thermoproteus tenax virus 1 (strain
<pre><(x){1,200}(L,I,V</pre>	YR/B_ECOLI	1
		YNU6_CAEEL ck: 431 len: 381 ! P50444 caenorhabditis elegans. hypothetical
<(X) {1,200} (L,I <(X) {1,200} (L,I x{95} (L)x(S) (MDIEFSQIHEMVYMH	1:	GAGEFEDFSKLSARQDARKTY1FTK1DGESEMIKKTKKALGVENESITUFLIKED. VHRIPISKPKCPDHLQKILQMIITSEADQVLSTKEPHPLRYLQVEKVNEVFGFEETLVLPDHTLFLDSDPFSRHPPITEGGGGGCPFM
r ck. 8893 len. 14	5	1
1: MQHUSYRWITLAIIS FFVSDNNNLRSANNEEKQSFQLSDILA LITEMYGMSLVAASYMGIVINKIFRAL	1: SVVYILLGILCWFFVSDNNN FTIYAILSYSTNYLTEMYGM	YNC9_CAEEL ck: 399 len: 336 ! P34542 caenorhabditis elegans. hypothetical
<pre>ck: 1867 len: 42 <(X){1,200}(L,I,V x{152}(V)x(T)(M)</pre>	1 YQCE_ECOLI	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(Cx(L)X(S)(L)X(S)(K)XX(V)XXX(S)X{153} 1: MLRSLSTISKSTVRCMSLTSKMAABQPSKQEVDDLFAEKPQHHNPEQRRHAYSVNKVELVGGVALD
JDKLLWRNWLRVLKNVWQQ	AGLPRLINTLRASGYDQLVL	YNA1_CAEEL ck: 5825 len: 170 ! P34496 caenorhabditis elegans. hypothetical
<(X){1,200}(L,1,V x{138}(A)x(S)(P 1: SVPGDPIDILWQQLAIL	1: NFGNAFLRADGRRDSDTPLT	1 <(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C x(82}(A)x(S)(L)xx(L)(S)(K)xx(I)xxx(S)x(41} 1: MMLINHTYKLLSYFLRKASNRFFNSSSSFSCSFLVFLFVVFFSDCFFSITSFLISFGILSSFLIF
N ck: 9681 len: 27	YPQQ_KLEPN	YN06_YEAST ck: 7226 len: 139 ! P53842 saccharomyces cerevisiae (baker's ye
1: MYNADVLAFGAHSDDVE MYNADVLAFGAHSDDVE PLINGYIEIVEAREKLYGKEAGVEYA	1: KSQFIPSKDSVSTPLTNGYI	<pre>1 <(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C</pre>
J ck: 3316 len: 22	YPJ	YM27_MARPO ck: 7679 len: 69 ! P38469 marchantia polymorpha (liverwort). h
ACREGE POSDY FOR VERROR	RGDELYHSICNWYDDYAQPLTIESH SAE RHOW RMAKARMILQKYHLSIHEVAQRCGFPDSDYFCRVFRRQF	<pre>1 <<(x){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C</pre>
x{156}(V)x(S)(L	١.	YKFF_ECOLI ck: 8141 len: 79 ! P75677 escherichia coli. hypothetical 9.0 k

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(L)xx(L)(C)(R)xx(V)xxx(P)x{113}
LEGGLVUMPQLLGRVWFASQPASLPVGSLCIDFPRLDIVLRGEYGNLL
SKLFAQHGTMRFIEYVRWV
2FGLTPGEYSARFQG
```

,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W) V)XX(I)(C)(R)XX(A)XXX(P)X(120) WEIGMGGTIAKFVKQEKKVMICDLTEAELSSNGTVSLRKEEAAEAARI YAEVSFPNGC 224 ! P42981 bacillus subtilis. hypothetical 2

! P27509 klebsiella pneumoniae. hypothetic

.V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W (P)XX(A)(T)(H)XX(A)XXX(C)X{117} TLKQLIAHSAGATRICCLSAADIERCREDKVLAMVAHIEGAGGFDGEGR ALGSDFDGITLPDELGDV

,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W (M)XX(P)(S)(R)XX(P)XXX(T)X{257} SFSGGVSFDLAYLRYIYQIPMAKFMGFSNTEIGLIMSTFGIAAIILYA LAYLRISTTWYCSMVIFGV ALCGPLGGIITTYSKVKSPTRVIQILSVLGLLTLTALLVTNSNPQSVA ! P77031 escherichia coli. hypothetical 46

41 ! P77136 escherichia coli. hypothetical 16

, V, M, A, P)X(P, T, S)(L, I, V, M, A, P)XX(L, I, V, M, A, F, Y, W I)xx(L)(S)(K)xx(L)xxx(L)x(30) DIVNSDSKKKPRIPLKKFLNAENVLTQTTSWTLNSRYVNVNSVNKVNV

, V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W (I)xx(V)(T)(R)xx(A)xxx(V)x{29} CRAFALRHNLVQLAERAGMNVQILRNKLNPSQPHLLTAPEIWLLTDLT ! P21316 escherichia coli. hypothetical 18

214 ! P45028 haemophilus influenzae. hypotheti

, V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W A)xx(V)(T)(R)xx(I)xxx(S)x{183} /LTAFLVTRTAIAETSPYVLMQQAADKLFSDIQANQSKIKQDPNYLRT

! P54434 bacillus subtilis. hypothetical 4

.V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W))xx(V)(T)(K)xx(L)xxx(L)x{16} (SLTKNLYLFWMCVMKMILVIGR

18 ! P95085 mycobacterium tuberculosis. hypot

,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W P)xx(A)(T)(R)xx(A)xxx(A)x{10} EDIDPDDGQRVLVDRIWPHGIRKDDQRVGIWCKDVAPSKELREWYHHQ

V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W (A)xx(I)(S)(R)xx(L)xxx(P)x{209} ALSEMGDYCVLPALLILSTYYHDYMVTSGVIVVRSIPMVFQPFLGVLV 94 ! P39642 bacillus subtilis. hypothetical 4

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(X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C) x(14}(I)x(T)(I)xx(T)(E)(C)(E)xxx(Y)x(244) x(14)(I)x(T)(I)xx(T)(E)(E)xxx(Y)x(244) x(244) x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (X){1,200}(L,I,V,M,A,P)X(P,T,S)(L,I,V,M,A,P)XX(L,I,V,M,A,F,Y,W)(C
x{99}(Y)x(T)(L)xx(V)(S)(R)xx(S)x{(249}

melspunstdosildaolelwhttearmksmalksaihlriadaihlhggaaslsoilskuhlps
glasdsoliudvalkosaeveogsissludvoggigaaaqaiskafphvkcsvldla
glasdsoliudvalkosaeveogsissludvoggigaaaqaiskafphvkcsvldla
hvvakapthtdvofiagdmfesippadavllksvlhdwdhddcvkilknckkaippreaggkviiinmvvgagpsdmkhkemqaifdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKLOFVPIOSENIKEAFOSFKEGLKEIKTNSFVLNAMFTMITMALLMGVVYSYFP
IVSRFLGDGEIGNFILIFCIGFGGFIGAALVSKWGFNNNRGLTYFTVLSIVSLALFLFTPIFAVSVIAAILFFIAMEYGEVLAKVKV
TATE THE TRANSPORTED TO SOCIO CONTRATA SOCIO CONTRA
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rotal length:
rotal sequences:
cpU time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Databases searched:
SWISS-PROT, Release 38.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _SEQUENCE 1.0
AAKG_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE; 95050763.

MEDILINE; 95050763.

MEDILINE; 95050763.

MITTERS L.A., KEMP B.E.;

THE T., HOUSE C.M., WITTERS L.A., KEMP B.E.;

THE T., HOUSE C.M., WITTERS L.A., KEMP B.E.;

THE T., HOUSE C.M., WITTERS L.A., KEMP B.E.;

"Mammalian 5'.AMP-activated protein kinase non-catalytic subunits are "Mammalian 5'.AMP-activated protein kinase non-catalytic subunits are "Mammalian 5'.AMP-activated protein kinase ";

Domologs of proteins that interact with yeast snfl protein kinase.";

J. Biol. Chem. 269:29343-29345(1994).

J. Biol. Chem. 269:29343-29345(1994).

SYNTHESIS by PHOSPHORYLATION OF ACCITYL-COA CARBOXYLASE. IT ALSO SYNTHESIS BY PHOSPHORYLATION AND REGULATES CHOLESTEROL SYNTHESIS VIA PHOSPHORYLATION AND REGULATES CHOLESTEROL SYNTHESIS AND ACT AS METABOLIC HYDROXYMETHYGLUTARYL-COA REDUCTASE. APPEARS TO ACT AS METABOLIC STREES-S-SENSING PROTEIN KINASE SWITCHING OFF BIOSYNTHETIC PATHWAYS WHEN CELULAR ATP LEVELIS ARE DEPLETED AND WHEN S'-AMP RISES IN WHEN CELULAR ATP LEVELIS ARE DEPLETED AND WHEN S'-AMP RISES IN RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA. THIS IS A REGULATORY RESPONSE TO FUEL LIMITATION AND/OR HYPOXIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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11-FEB-1995 (Rel. 31, Last sequence update)
12-DEC-1998 (Rel. 37, Last annotation update)
13-AUP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN)
138 KD SUBUNIT) (FRAGMENTS).
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                                                                                                                                                        DOMAIN
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SIMILARITY: BELONGS TO THE 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA SUBUNIT FAMILY.
SUBUNIT FAMILY.
SIMILARITY: CONTAINS 4 CBS DOMAINS.
M: PEO0571; CBS: 1.
M: PEO0571; CBS: 1.
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                                                                                                       EMBL; U59433; AAC44308.1; -.

EMBL; D64116; BAA10975.1; -.

EMBL; D29112; CAB13465.1; -.

HSSP; P02901; IACP;
SUBTILIST; B611536; ACPA.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.

PROSITE; PS00075; ACP_DOMAIN; 1.

PROSITE; PS50075; ACP_DOMAIN; 1.

PRAM; PF00550; pp-binding; 1.

PRAM; PF00550; pp-binding; 1.

PFAM; PF00550; pp-binding; 1.

PFAM; PF00550; pp-binding; 1.

PFAM; PF00550; pp-binding; 1.

PFAM; PF005F05ANTETHEINE.

Fatty acid biosynthesis; Phosphopantetheine.

Fatty acid biosynthesis; Phosphopantetheine.

PFAM; PF00550; pp-binding; 1.
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Bacillus subtilis.
Bacteria; Firmicutes;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
ACYL CARRIER PROTEIN (ACP).
SEQUENCE OF 15-77, AND SEQUENCE OF 1-14 FROM STRAIN-168;
                                                                                                                                                                               MEDIINE; 96326321.
MORBIDONI H.R., DE MENDOZA D., CRONAN J.E.
"Bacillus subtilis acyl carrier protein is
lipid biosynthesis genes.";
J. Bacteriol. 178:4794-4800(1996).
                                                                                                                                                                                                                                                             aacteria; Firmicutes; Bacillus/Clostridium group;
aacillus/Staphylococcus group; Bacillus.
                                                                                                                              OGURO A., KAKESHITA H.,
Submitted (MAR-1996) to
                                                                                                                                                           EQUENCE FROM N.A.
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DE ALANINE RACEMASE (E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila mojavensis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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ALCOHOL DEHYDROGENASE 2 (EC 1.
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P09369;
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(EC 5.1.1.1).
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FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G., DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T. MCDONALD L., ARTLACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O., PETER J.C.;
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Bacteria;
                                                                                                                                                                                                                               SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Partial sequence of alanine racemase from Treponema pallidum."; submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-ALANINE - D-ALANINE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis spirochete."; Science 281:375-388(1998).
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STRAIN-NICHOLS;
MEDLINE; 98332770.
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PFAM; PF00842; Ala_racemase;
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                                                                                                                                                                                                                                                                                                                VERVYIR
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Spirochaetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                    ILPIGYADGV
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AMIA

PRECURSOR

Enterobacteriaceae;

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RANGE PRODUCTION OF THE PRODUCT OF T
I AA_SEQUENCE 1.0
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gene of Salmonella typhimurium.";
J. Bacteriol. 175:4990-4999(1993).
J. Bacteriol. 2007 Bacteriol. 175:4990-4999(1993).
J. CATALYTIC ACTIVITY: HYDROLYZES THE LINK BETWEEN N-ACETYLMURAMOYL.
RESIDUES AND L-AMINO ACID RESIDUES IN CERTAIN BACTERIAL CELL-WALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XU K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STYGENE; SG10008; AMIA.
PFAM; PF01520; Amidase_3; 1.
Hydrolase; Cell wall; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990
01-NOV-1990
15-DEC-1998
                                                                                                                                                      "Nucleotide sequence of the Serratia marcescens SR50 chromosomal ampC beta-lactamase gene.";
FEMS Microbiol. Lett. 58:295-299(1990).
FEMS MICROBIOL. THIS PROTEIN IS A SERINE BETA-LACTAMASE WITH A SUBSTRATE
SPECIFICITY FOR CEPHALOSPORINS.
-i- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)0 = A SUBSTITUTED BETA-
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-SR50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serratia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                         This
                                                                                                                                                                                                                                                                                                                     MEDLINE; 91032898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serratia.
                                                                           -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
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SWISS-PROT entry is copyright. It is produced een the Swiss Institute of Bioinformatics and
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(Rel. 16, Last sequence update)
(Rel. 37, Last annotation update)
ASE PRECURSOR (EC 3.5.2.6) (CEPHALOSPORINASE).
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                                                              PERIPLASMIC (BY SIMILARITY).

O THE CLASS-C BETA-LACTAMASE FAMILY.
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PROBABLE N-ACETYLMURAMOYL-L-ALANINE
AMIDASE AMIA.

55107FEC CRC32;
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         through a collaboration -
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ACT_SITE
BINDING
SEQUENCE
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01-APR-1993
01-JUN-1994
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MEDLINE; 93199292.

MOPP U., WIEDEMANN B., LINDQUIST S., NORMARK S.;

MOPP U., WIEDEMANN B., NORMARK S.;

MOPP U., WIEDEMANN B., NORMARK S.;

MOPP U., WIEDEMANN B., NORMARK S.;

MOPP U., NORMARK S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
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PROSITE; PS00336; BETA_LACTAMASE_C; 1.
PPAM; PF001144; beta-lactamase; 1.
Hydrolase; Antibiotic resistance; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X52964; CAA37137.1; -
                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 93199292.
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Citrobacter
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EMBL; Z14002; CAA78390.1;
EMBL; Z14003; CAA78391.1;
PIR; A48901; A48901.
PIR; S26138; S26138.
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A48176; A48176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
79
328
376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTAMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASKQTGKPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANYAQGYSKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25, Created)
25, Last sequence 29, Last annotations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacter cloacae.
gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKPVRVNPGP
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BY SIMILARITY.
SUBSTRATE (BY SIMILARITY);
016BEF00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDAESYGIKS
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                                                                                                                                                                                     Gene 104:259-264(1991).

Gene 104:259-264(1991).

Gene 104:259-264(1991).

Gene 104:259-264(1991).

Gene 104:259-264(1991).

Gene 104:259-264(1991).

FUNCTION: CALCIUM IS GREATLY ENHANCED BY ANIONIC PHOSPHOLIPIDS.

IT BINDS TWO CALCIUM IONS WITH HIGH AFFINITY.

SUBUNIT: TETRAMER OF 2 LIGHT CHAINS (P10 PROTEINS) AND 2 HEAVY CHAINS (P36 PROTEINS).

IT SUBCELLULAR LOCATION: IN THE LAMINA BENEATH THE PLASMA MEMBRANE.

IT TISSUE SPECIFICITY: ADDUT BRAIN, HEART, STRIATED MUSCLE, LIVER, KIDNEY, AND VERY HIGH LEVELS IN SKIN.

CONSTANT LEVELS DURING EARLY EMBRYOGENESIS, AND IN MATURE EGGS.

CONSTANT LEVELS DURING EARLY EMBRYOGENESIS, AND IN CREASES AT 8H. AFTER MIDBLASTULA TRANSITION, THE STEADY STATE LEVEL INCREASES SUBSTANTIALLY.

DOMAIN: CONTRAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.

HISCELLANEOUS: IT MAY CROSS-LINK PLASMA MEMBRANE PHOSPHOLIPIDS WITH ACTIN AND THE CYTOSKELETON AND BE INVOLVED WITH EXCCYTOSIS.

1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S261
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminus.
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01-AUG-1992 (Rel. 23, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ANNEXIN II TYPE II (LIPOCORTIN II) (CALPACTIN (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL IV) (PAP-IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Ewp non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92011609.
IZANT J.G., BRYSON L.J.;
"Xenopus annexin II (calpactin I) heavy terminus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHAPADA).
IV) (PAP-IV).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92009222.
GERKE V., KOCH W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primary structure and nnexin II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLLENGWLVD ARHVPSPHHD CRPEDEKPTL LVVHNISLPP GEFGGPWIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S26139; S26139
ENCE 187 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSIGIELEGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EL C.; expression of the Xenopus laevis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSRFHAMLTT
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ANTICOAGULANT PROTEIN
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Xenopodinae;
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EMBL; M58575; AAA49664.1; EMBL; M58576; AAA49665.1; EMBL; M60769; AAA49886.1; PIR; JQ1298; JQ1298.

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IIAA_SEQUENCE 1.0

IID ARG1_XENLA
AC Q91553;
DT Q1-NOV-1997 (R
DT 01-NOV-1997 (R
DT 01-NOV-1999 (R
DT 15-JUL-1999 (R
DE ARGINASE, NON-
ON Xenopus laevis
OC ELEVETONE FROM
RC TISSUE-INTESTINE
RN [1]
RX MEDLINE; 95014
RA PATTERTON D.,
RT "THYFOLD hONITH
RT AIGHTOLON:
CC -!- COFACTION:
CC -!- COFACTION:
CC -!- SUBUNIT:
CC -!- TISSUE SP)

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                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE NITESTINE;

X MEDLINE; 95014323.

A PATTERTON D., SHI Y.-B.;

Thyroid hormone-dependent differential regulation of multip
"Thyroid hormone-dependent differential regulation of multip
"Th
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HSSP; P04083; 1809.

PROSITE; P$00223; ANNEXIN; 4. PRAM; P$00191; annexin; 4. Pram; P$00191; annexin; 4. Pram; P$00191; annexin; 6. Pram; P$0 Pram; P$0 Pram; P$0 Pram; P$10 Pram; P$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
MOD_RES
VARIANT
VARIANT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
RAGINASE, NON-HEPATIC 1 (EC 3.5.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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                                     DEVELOPMENTAL STAGE: FIRST DETECTED IN NEURULA (STAGE 16/17).
HIGHEST LEVELS IN WHOLE TANDELE FOUND BAROUND STAGE 47/48. IN THE
INTESTINE, INCREASED LEVELS ARE FOUND DIRING METAMORPHOSIS (STAGES
S8-64). LOW LEVELS EXPRESSED IN HINDLIMB UNTIL STAGE 66 AFTER
WHICH, LEVELS DRAMATICALLY INCREASE. IN THE TAIL, A CONSTANT HIGH
LEVEL OF EXPRESSION IS FOUND THROUGHOUT METAMORPHOSIS.
INDUCTION: ACTIVATED BY THYROID HORMONE (T3).
SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
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B41002;
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Xenopodinae;
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METAMORPHOSIS.
INDUCTION: ACTIVATED
SIMILARITY: BELONGS '

ACTIVATED BY THYROID HORMONE (T3).

BELONGS TO THE ARGINASE FAMILY.

INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS (STAGES 58-64) AND IN THE HINDLINE, EXPRESSED AT LOW LEVELS DURING METAMORPHOSIS UNTIL STAGE 66 WHEN LEVELS DRAMMATICALLY INCREASE. IN THE TAIL, A CONSTANT HIGH LEVEL OF EXPRESSION IS FOUND THROUGHOUT

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ARG1_XENLA Length: 360
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TISSUE-INTESTINE;

X MEDILINE; 95014323.

A PATTERTON D., SHI Y.-B.;

A PATTERTON D., SHI Y.-B.;

Tribyroid hormone-dependent differential regulation of my ribyroid hormone-dependent in THE UREA CYCLE, MAIL IN TISSUE REMODELING.

-!- CORACTOR: MANGANESE (BY SIMILARITY).

-!- CORACTOR: MANGANESE (BY SIMILARITY).

-!- PATHWAY: FIRST STEP IN ARGININE DEGRADATION.

-!- TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE.

-!- TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE.
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ARG2_XENLA
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01-NOV-1997 (Rel. 35, Last and
01-NOV-1997 (Rel. 35, Last and
ARGINASE, NON-HEPATIC 2 (EC 3.
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                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
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TAIL.
DEVELOPMENTAL STAGE: FIRST DETECTED IN NEURULA (STAGE 16/17).
HIGHEST LEVELS IN WHOLE TADPOLE FOUND AROUND STAGE 47/48. IN THE
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EC 3.5.3.1)
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ANAGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 1 (BY SIMILARITY).

MANGANESE 1 AND 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).

MANGANESE 2 (BY SIMILARITY).
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ARG2_XENLA Length: 360
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                                                                                                                                                                                                          _SEQUENCE 1.0

ARG3_XENLA
Q91555;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
ARGINASE, NON-HEPATIC 3 (EC 3.5.3.1).
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HSSP; P07824; 2RLA.
HSSP; P07824; 2RLA.
PROSITE; PS00147; ARGINASE_1; 1.
PROSITE; PS00148; ARGINASE_2; 1.
PROSITE; PS01053; ARGINASE_3; 1.
PFAM; PF00491; arginase; 1.
PFAM; PF00491; Arginase metabolism; Hydrolase; Manganese;
Urea cycle; Arginine metabolism; Hydrolase; Manganese;
351
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                      LHGQPVSFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122 M
1145 M
1147 K
149 K
253 K
39154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 14, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDLHFSKVPN DELYNSIVKH
                                                                                                                                                                                                                                                                                                                                                                   GGLTYREGVY
                                                                                                                                                                                                                                                                                                                                                                                                                       RELQDKVPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
26CE48BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08:02 Type: P Check:
                                                                                                                                                                                                                                                                                                                                                                                                                       PGFSWAKPCL
                                                                                                                                                                                                                                                                                                                                                                   ITEEIHNTGM
                            UREA CYCLE, MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIWVDAHADI
                                                                                                                                                                                                                                                                                                                                                                     LSAVDLVEVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRTVGLACKV
                                                                  0f
                                                                                                                                                           Amphibia;
Xenopodinae;
                                                                  multiple
                              BE INVOLVED
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RRR OCC OGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGC_ECOLI
P11446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
METAL
METAL
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SEQUENCE
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                                                                                              01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE (EC 1.2.
ACETYL-GLUTAMATE SEMIALDEHYDE DEHYDROGENASE) (NAGSA
                                                                                                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urea cycle; Ar
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                                                                    Escherichia coli
                                                                                                                                                                                                                                                            301
                                                                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00147; ARGINASE_1;
PROSITE; PS00148; ARGINASE_3;
PROSITE; PS01053; ARGINASE_3;
PFAM; PF00491; arginase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U08408; AAA56893.1; -. HSSP; P07824; 2RLA.
SEQUENCE FROM N.A. MEDLINE; 89121510.
                                         Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: MANGANESE (BY SIMILARITY).

PATHMAY: FIRST STEP IN ARGININE DEGRADATION.
SUBUNIT: HOMOTRIKER (BY SIMILARITY)

TISSUE SPECIFICITY: EXPRESSED AT DIFFERING TADPOLE STAGES IN
TAIL, INTESTINE, HINDLIMB AND TRUNK REGION. STRONGEST IN TADPOLE
TAIL.

DEVELOPMENTAL STAGE: FIRST DETECTED IN EARLY TAILBUD (STAGE
23/24). HIGHEST LEVELS IN WHOLE TADPOLE FOUND AROUND STAGE 47/48.
23/24). HIGHEST LEVELS IN WHOLE TADPOLE FOUND AROUND STAGE 47/48.
IN THE INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS
IN THE INTESTINE, INCREASED LEVELS ARE FOUND DURING METAMORPHOSIS
(STAGES 58-64) AND IN THE HINDLIMB, EXPRESSED AT LOW LEVELS DURING
METAMORPHOSIS.

METAMORPHOSIS.

METAMORPHOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDICTION: ACTIVATED BY THYROID HORMONE (T3).
SIMILARITY: BELONGS TO THE ARGINASE FAMILY.
                                                                                                                                                                                                                               ESDNEEQVRI
                                                                                                                                                                                                                                                             PVLATTSEEV
                                                                                                                                                                                                                                                                                          SFDIDAFDPA
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                                                                                                                                                                                                                                                                                                                      RDLDPAEQFI
                                                        Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arginine metabolism; Hydrolase; Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   LKKQVNIIKL QKKCSHSVAV
                                                                                                                                                                                                                                                                                                                      LKNYNISYYS
                                                                                                                                                                                                                                                                                                                                                LHGQPVSFLL
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                                                                                                                                                                                                                                                                                          LAPATGTPVI
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145
147
149
253
255
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                                                        gamma
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MANGANESE
MANGANESE
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MANGANESE
MANGANESE
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A896B3FA
                                                        subdivision; Enterobacteriaceae
                                                                                                                                                                                      334
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SE 1 AND 2 (BY SIMILARITY).

SE 2 (BY SIMILARITY).

SE 1 (BY SIMILARITY).

SE 1 AND 2 (BY SIMILARITY).

SE 2 (BY SIMILARITY).

SEA CRC32;
                                                                                                                                                                                                                                                             GAHTRADTII DVLPTPSTSY
                                                                                                                                                                                                                                                                                                                      KVMEKTFDQL
                                                                                                                                                                                                                                                                                                                                                  PGFSWAKPCL
                                                                                                                                                                                                                                                                                                                                                                            GHAQQCPDLC
                                                                                                                                                                                                                                                                                                                                                                                                         DEQYNSIVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                     IGAPFSKGQK RRGVEHGPAA
                                                                                                                                                                                                                                                                                          ITEEIHNIGM LSALDLVEVN
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VPGCYPTAAQ

PGVDVVFLAT THQYPELLEQ LLDLNQWPVI

NATSGVSGAG

51

QLKGIVDLPL QPMSDISEFS

ATFYEKYYGF LALKPLIDAD MLNTLIVGAS

GYAGAELVTY

VNRHPHMNIT ALTVSAQSND

AGKLISDLHP

AHEVSHDLAP

251

VTQAQVAQVL QQAYAHKPLV RLYDKGVPAL KNVVGLPFCD

IGFAVQGEHL

QFLEAGCVVF
NKLKEANLIA
RKAAISNSFC
ETITCRLKSG

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ARGC_ECOLI
                                          EMBL; M21446; AAA23477.1;

EMBL; J01887; AAB59146.1;

EMBL; X55417; -; NOT_ANNOTATED_CDS.

EMBL; U00006; AAC43064.1;

EMBL; D00006; AAC43064.1;

EMBL; AE000470; AAC76940.1;

PIR; J70332; RDECEP.

ECOGENE: E010065; ARGC.

ECOGENE: E010065; ARGC.; 1.

PRASTTE: P801224; ARGC; 1.

PFAM; PF01118; Semialdhyde_dh; 1.

AIGINIAD blosynthesis; Oxidoreductase; NADP.

ACT_SITE 154 154 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        MEINNEL T., SCHMITT E., MECHULAM Y., BLANQUET S.;

Structural and biochemical characterization of the Escherichia arge gene product.";

J. Bacteriol. 174:2323-2331(1992).

-I. CATALYTIC ACTIVITY: N.-ACETYL-1-GLUTAMATE 5-SEMIALDEHYDE + N.-ACETYL-5-GLUTAMYL PHOSPHATE + NADPH.

-I. PARHWAY: THIRD STEP IN ARGININE BIOSYNTHESIS.

-I. SIMILARITY: TO OTHER BACTERIAL ARGC AND TO NAGSA DOMAIN OF PROTEIN ARG5,6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94089392.
BLATTNER F.R., BURLAND V.D.,
DANIELS D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARSOT C., BOYEN A., COHEN G.N., GLANSDORFF N.;
"Nucleotide sequence of Escherichia coli argB and
comparison of N-acetylglutamate kinase and
N-acetylglutamate-gamma-semialdehyde dehydrogenase
and analogous enzymes.";
Gene 68:275-283(1988).
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 83143275.

PIETTE J., CUNIN R., BOYEN A., CHARLIER D.R.M., CRABEEL M.,
VAN VLIET F., GLANSDORFF N., SQUIRES C., SQUIRES C.L.;
"The regulatory region of the divergent argECBH operon in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DANIELS D.L.;

DANIELS D.L.;

"Analysis of the Escherichia coli genome. IV. DNA sequence region from 89.2 to 92.8 minutes.";

Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-19
STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-48 FROM N.A. STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 10:8031-8048(1982).
Length: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92202162
                               334 AA;
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                            154 E
; 35952 MW;
February 14, 2000 08:02
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                                 DB98AB60 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase with homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III,
Type: P Check:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  argC genes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
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MBL outstation .
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IIVATEDNLL

KGAAAQAVQC

ANIRFGYAET

ITSD

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A MADDLINE; 95213032.

WANDLINE; 95213032.

A YAN W.L., LERNER T.J., HAINES J.L., GUSELLA J.F.;

AN WALL, LERNER T.J., HAINES J.L., GUSELLA J.F.;

RT "Sequence analysis and mappling of a novel human mitochondrial ATP

RT Sequence analysis and mappling of a novel human mitochondrial ATP

RT Sequence analysis and mappling of a novel human mitochondrial ATP

RT Sequence analysis and mappling of a novel human mitochondrial ATP

RT Sequence analysis and mappling of a novel human mitochondrial ATP

RT Sequence analysis and mappling of a novel human CP(1) - THE CATALYTIC

CC MEMBRANE COMPONENT (F0) OF MITOCHONDRIAL ATPASE.

CC -!- SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

CC -!- SUBCLILULAR LOCATION: MITOCHONDRIAL MEMBRANE.

CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE.

CC -!- MISCELLANEOUS: THERE ARE THREE GENES WHICH ENCODE THE

MITOCHONDRIAL ATP SYNTHASE PROTECLIPID AND THEY SPECIFY PRECURSORS

CC WITH DIFFERENT IMPORT SEQUENCES BUT IDENTICAL MATURE PROTEINS.

CC -!- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.

CC --- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                        OSCHOOLS
                                                                                                                                                                                                                                                                                                                               AT93_HUMAN Length: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
AT93_HUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P48201;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ATP SYNTHASE LIPID-BINDING PROTEIN P3 PRECURSOR (EC 3.6.1.34) (ATPASE PROTEIN 9) (SUBUNIT C).
ATP5G3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        SEQUENCE 1.0
                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00605; ATPASE_C; 1.
PFAM; PF00137; ATP-synt_C; 1.
Hydrogen ion transport; Lipid-binding; Mitochondrion;
Transit peptide; Multigene family; Transmembrane.
TRANSIT 1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U09813; AAA78807.1; -. MIM; 602736; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                      01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
Podospora anserina Mitochondrion.
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                                                                                                                                                                                                                                                      GVSQLIQREF
                                                                                                                                                                                                                                                                                             MFACAKLACT
                                                                                                                                                        PODAN
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142 AA;
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                                                                                                                                                        STANDARD;
                                                                                                                                                                                                               QQLFSYAILG
                                                                                                                                                                                                                                                      QTSAISRDID
                                                                                                                                                                                                                                                                                           PSLIRAGSRV
                                                                                                                                                                                                                                                                                                                                 February 14, 2000 08:02 Type: P
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                                                                                                                                                                                                                                                      TAAKFIGAGA
                                                                                                                                                                                                                  FALSEAMGLF
                                                                                                                                                                                                                                                                                             AYRPISASVL
                                                                                                                                                                                                                                                                                                                                                                                           ATP SYNTHASE
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                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                      PP SYNTHASE LIPID-BINDING PROTEIN. 7D215F04 CRC32;
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| | IAA_SEQUENCE 1.0
| ATPR_PONPA
| AC P92564;
| DF 01-NOV-1997 (F
| DF 01-NOV-1997 (F
| DF 01-NOV-1997 (F
| DF 01-NOV-1997 (F
| DF 01-NOV-1999 (F
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                                                                                                                                                                                                                                                                                                                                                                                                         Hydrogen
TRANSMEM
SEQUENCE
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or send an email to license@isb-sib.ch).
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MEDLINE; 90291512.
CUMMINGS D.J., MCNALLY K.L., E
The complete DNA sequence of
anserina.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUTT. Genet. 17:375-402(1990).

-i- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYM.

-i- SUBCULIAR LOCATION: MEMBRANE-BOUND.

-i- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fu
Sordariales;
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus abelii (Sumatran Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993694, 1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
ATP SYNPHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
MTAIP8 OR ATP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X55026; CAA38808.1; -.
Hydrogen ion transport; CF(0); Mitochondrion;
TRANSMEM 13 32 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
      EMBL; X97707; CAA66287.1;

PFAM; PF00895; ATP-Synt_8;

Hydrogen ion transport; CI

TRANSMEN 8 24

SEQUENCE 68 AA; 7860 MV
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=YN93-312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Eutheria; Primates;
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s; Sordariaceae; Pod
                                                          transport; CF(0); Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5944 MW;
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            7860 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D3E7DF1F CRC32;
            B5CEA057
                                    POTENTIAL
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               CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on ng as its content is in no
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ATP8_PONPA

Length: 68

February

14,

2000 08:02

Type:

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3336

PHSLPPQY TIITPMLLAL

MPQLUTTTWP

FLITQLKLLN

SHLHPPTPPK

FTKPKLHAKP

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ATP8_PONPP
EQUENCE FROM N...

**BOUENCE FROM N...

**MEDLINE; 95132634.

**HORAI S., HAYASAKA K., KONDO R., TSUcanal Processor of the structure of the structure of the structure of the structure of hominoid mitochondrial DNAs. ";

**Proc. Natl. Acad. Sci. U.S.A. 92:532-536(1995).

-!- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

**COMPANY OF THE MITOCHONDRIAL ATPASE COMPLEX.**

**COMPANY OF THE MITOCHONDRIAL ATPASE COMPLEX.**

**COMPANY OF THE MITOCHONDRIAL ATPASE PROTEIN 8 FAMILY.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ATP_SYNTHASE_PROTEIN 8 (EC 3.6.1.34) (A6L).
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                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTATP8
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XVX.. ARNASON U.;

The mitochondrial DNA molecule of Sumatran orangutan and a molecular Tree mitochondrial DNA molecule of Sumatran orangutan and a molecular proposal for two (Bornean and Sumatran) species of orangutan.";

J. MOL. BYOL. 43:431-437(1996),

FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.

SUBCELLULAR LOCATION: MEMBRANE-BOOTEIN 8 FAMILY.

SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Mitochondrion
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01-NOV-1997 (Rel. 35, Last seq
15-JUL-1999 (Rel. 38, Last ann
ATP SYNTHASE PROTEIN 8 (EC 3.6
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pF00895; ATP-synt_8; 1.
pF00895; ATP-synt_8; 1.
ygen ion transport; CF(0); Mitochondrion;
gen ion transport; CF(0); Mitochondrion; Mitochondrion;
gen ion transport; Mitochondrion; Mitochon
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LPONPP
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Catarrhini; Hominida
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(A6L).
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!!AA_SEQUENCE 1.0
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                                                                                                                                                                 MEDDINE: 93162045.

MEDDINE: 93162045.

HOCHSTRASSER D.F., FRUTIGER S., PAQUET N., BAIROCH A., RAVIER F., PASCUALI C., SANCHEZ J.-C., TISSOT J.-D., BJELLQVIST B., VARGAS R., PASCUALI C., SANCHEZ J.-C., TISSOT J.-D., BJELLQVIST B., VARGAS R., PASCUALI C., SANCHEZ J.-C., TISSOT J.-D., BJELLQVIST B., VARGAS R., PAPPEL R.D., HUGHES G.J.;

"Human liver protein map: a reference database established by microsequencing and gel comparison.";

Electrophoresis 13:992-1001(1992)

-I-FUNCTION: PRODUCES ATP FROM AND FIN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE.

-I-SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

SEEMS TO HAVE NINE SUBUNITS: A, B, C, D, E, F, G, F6 AND 8 (OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

LAMBERDIN J.E., MCCREADY P.M., SKOWRONSKI E., ADAMSON A.W.,

BURKHART SCHULTZ K., GORDON L., KYLE A., RAMIRRZ M., STILWA-

BURKHART SCHULTZ K., GORDON L., BANGANAN L., POUNDSTONE P.,

CHRISTENSEN M., GEORGESCU A., AVILA J., LIU S., ATTIX C.,

TRANKHEIM M., AMICO-KELLER G., COEFIELD J., DUBATTE S., LUCA-

BRUCCE R., THOMAS P., QUAN G., KRONMILLER B., ARELLANO A.,

MONTGOMERY M., OW D., NOLAN M., TRONG S., KOBAYASHI A., OLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-LI
MEDLINE;
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SEQUENCE FROM N.A.
MEDLINE; 92182007.
JORDAN E.M., BREEN G.A.M.;
MOLECULar cloning of an import precursor of human mitochondrial ATP synthase complex.";
human mitochondrial ATP 130:123-126(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MONTGOMERY M., OW D.,
CARRANO A.V.;
Submitted (FEB-1998) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP5D.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Primates; Catarrhini; Hominid
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 23-38.
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01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
APP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D38115; BAA07309.1; PFAM; PF00895; ATP-synt_8
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MITOCHONDRIAL PRECURSOR (EC 3.6.1.34).
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STILWAGEN S.,
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its

LOCATION: MITOCHONDRIAL.
BELONGS TO THE ATRASE EPSILON CHAIN FAMILY.

TO THE

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STING CREEK 
                                                                                                                                                                                                                                                                                                                      ATPZ_BACP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHTA S., YOHDA M., ISHIZUKA M., HIRATA H., HAMAMOTO T.,
OTHWARA-HAMAMOTO Y., MATSUDA K., KAGAWA Y.;
"Sequence and over-expression of subunits of adenosine triphosphate
synthase in thermophilic bacterium PS3 ";
Blochim. Blophys. Acta 933:141155(1988)
-i- FUNCTION: A POSSIBLE FUNCTION FOR THIS PROTEIN IS TO GUIDE THE
ASSEMBLY OF THE MEMBRANE SECTOR OF THE ATPASE ENZYME COMPLEX.
-I- SIMILARITY: TO THE CORRESPONDING SUBUNIT IN OTHER BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATPZ_BACP3
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EMBL; X63423; CAA45017.1; -.
EMBL; AC004221; AAC04304.1; -
PIR; S22348; S22348.
SWISS-2DPAGE; P30049; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires or send an email t
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01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 35, Last annotation update)
01-MOV-1997 (Rel. 35, Last annotation update)
ATP SYNTHASE PROTEIN I.
Bacillus P3 (Thermophilic bacterium PS-3).
Bacteria; Firmicuttes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase;
Mitochondrion; Transit peptide.
TRANSIT 1 22 MITOCHONDRION.
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                                                                                   101
                                                                                                                                                                                                                                                                                                                      EMBL; X07804; CAA30647.1; -. 
PIR; S01397; S01397; S01397; Hydrogen ion transport; CF(0); SEQUENCE 127 AA; 14595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
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168 AA;
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0182AE71 CRC32;
PRT;
                                                                                                                                                                                                                                                                                                                   Transmembrane.
5999D881 CRC32;
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398
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BMPA_XENLA
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EMBL; X63424; CAA450.8.1; -.
PIR; S16244 S16244
PIR; JH0687; JH0687.
HSSP; p18075; IBMP.
PROSITE; PS00250; TGF_BETA; 1.
PFAM; PF00019; TGF-beta; 1.
PFAM; PF00688; TGFb_propeptide; 1.
S1gnal; Growth factor; Cytokine; B.
S1GNAL 1
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01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-UIL-1993 (Rel. 26, Last annotation update)
01-UIL-1993 (Rel. 26, Last annotation update)
BONE MORPHOCENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).

Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                     DISULFID
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DISULFID
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CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsendan.email.tolicense@ibb-sib.ch).
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MEDLINE; 91274367.
PLESSOW S., KOESTER M., KNOECHEL W.;
"CDNA sequence of Xenopus laevis bone morphogenetic (BMP-2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iochim. Biophys. Acta 1089:280-282(1991).
SLTPDKDNWP QIRPLLYTFS HDGKGHALHK RQKRQARHKQ
                                                                                                                                                                       FELRLISMEG LKRRPTPGKN VVIPPYMLDL
                                                                                                                                                                                                                  MVAGIHSLLL LLFYQVLLSG CTGLIPEEGK RKYTESGRSS
                                                                                    ELRIFREQVQ
                                                                                                                                                                                                                                                              Length: 398 February 14, 2000 08:02
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298
3327
2027
1137
1167
                                         VTPAIARWIA HKQPNHGFVV
                                                                                    EPFESDSSKL
                                                                                                                                                                                                                                                                                                          45575 MW;
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BONE MORPHOGENETIC PROTEIN 2
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POTENTIAL.
POTENTI
                                                                                       HRINIYDIVK
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                                                                                                                                                                            YHLHLAQLAA
                                                                                       PAAAASRGPV
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                                                                                    VRLLDTRLVH
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HPLYVDFSDV GWNDWIVAPP GYHAFYCHGE CPFPLADHLN STNHAIVQTL

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SIGNAL
PROPEP
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Ol-JUL-1993 (Rel. 26, Created)

Ol-JUL-1993 (Rel. 26, Last sequence update)

Ol-JUL-1993 (Rel. 26, Last annotation update)

BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 92378616.
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TF000019; TGF_beta; 1.

PF00688; TGFb_propeptide; 1.

L; Growth factor; Cytokine; E
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                                        ACCVPTELSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             45616 MW;
                                   ISMLYLDENE KVVLKNYQDM VVEGCGCR
                                                                            GYHAFYCHGE CPFPLADHLN STNHAIVQTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.

POTENTIAL.
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                                                                                      BR3A_HUMAN STANDARD;

Q01851; Q15318; Q14986;

Q1-UL-1993 (Rel. 26, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-NOV-1997 (Rel. 35, Last annotation update)

Q1-NOV-1997 (Rel. 35, Last annotation update)

BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (B
(HOMEOBOX/POU DOMAIN PROTEIN RDC-1)

FOU4F1 OR BRNJA OR RDC1.

HOMO Sapiens (Human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebra
SEQUENCE FROM N.A.
TISSUE-RETIKA;
XIANG M., ZHOU L.-J., MACKE J.P., EDDY R.L., S
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                    251
                                                                    Eutheria;
[1]
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aromatic hydrocarbons catabolism; Oxidoreductase; NAD NP_BIND 9 3 NAD (BY SIMILARITY).
SECULENCE 153 153 BY SIMILARITY.
SECULENCE 275 AA; 28726 MW; EA999DF7 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BPHB_PSEPS STANDARD; PRT; 275 AA.

P08694;

01-JAN-1988 (Rel. 06, Created)

01.NOV-1991 (Rel. 20, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation update)

BIPHENYL-2,3-DIHYDRO-2,3-DIOL DEHYDROGENASE (EC 1.3.1.-) (BIPHENYL-CLS-DIOL DEHYDROGENASE)

CIS-DIOL DEHYDROGENASE) (2,3-DIHYDROXY-4-PHENYLHEXA-4,6-DIENE
                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M15333; AAA25752.1; ALT_INIT.
HSSP; P47227; 1BDB.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-KF707;
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Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                                                                             GGLGVRGFFS GAGGNDLLEQ LNIHP
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                                                                                                                                                                                                                                                                                                                                                                              NVLGIVGDVR
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                                                                            Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; ADH_SHORT; 1. adh_short; 1.
                                                                                                                                                                                                                                                                                                                 VGLVRELAFE LAPYVRVNGV GPGGMNSDMR GPSSLGMGSK
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                                                                      Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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 SHOWS T.B., NATHANS
J databases.
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SEQUENCE FROM N.A.

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MEDLINE; 94052142.

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MEDLINE; 94052142.

MEDLINE; 94052142.

MEDLINE; 94052142.

METHORITHMENT OF THE POUT FAMILY OF THE POUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developing mammalian nervous system.";

Nucleic Acids Res. 20:4919-4925(1992)

-i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR WHICH MAY PLAY A ROLE IN FUNCTION: PROBABLE TRANSCRIPTION FACTOR WHITHIN A SUBSET OF THE REGULATION OF SPECIFIC GENE EXPRESSION WITHIN A MAINTAINING THE IDENTITIES OF A SMALL SUBSET OF VISUAL SYSTEM NEURONS.

-i- SUBCCLLULAR LOCATION: NUCLEAR.

-i- TISSUE SPECIFICITY: BRAIN. SEEMS TO BE SPECIFIC TO THE RETINA. PRESENT IN THE DEVELOPING BRAIN, SPINAL CORD AND EXE.

-i- DEVELOPMENTAL STAGE: EXPRESSION PEAKS EARLY IN EMERYOGENESIS (DAY 13.5) AND IS UNDETECTABLE 14 DAYS AFTER BIRTH.

-i- SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
   CONFLICT
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EMBL; U10062; AAA57161.1; JOINED.
EMBL; L20433; AAA65605.1; -.
EMBL; X64624; CAAA5907.1; -.
HISSP, P10037; 1AU7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a cleaver the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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PFAM; PF00157; pou; 1.
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PROSITE; PS00035; PCU_1; 1.
PROSITE; PS00465; PCU_2; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
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novel POU homeodomain gene specifically expressed in cells of the
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           WW;
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GAG -> ARR (IN REF 2).

MISSING (IN REF 3).

MISSING (IN REF 3).

GB -> AR (IN REF 3).

GP -> PR (IN REF 3).

GP -> AR (IN REF 3).

GP -> AR (IN REF 3).

G -> A (IN REF 3).

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           R (IN REF. 3)
> GS (IN REF.
> PS (IN REF.
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BL outstation -
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BR3A_HUMAN Length: 423
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BRALLBRAFI STAN
Q17134;
Q17134;
Q1-100v-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
D1-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLIADD P. W.H.) KOSCHORZ B., HOLLAND L.Z., HERRMAN HOLLAND P.W.H.) KOSCHORZ B., HOLLAND L.Z., HERRMAN "Conservation of Brachyury (T) genes in amphioxus developmental and evolutionary implications."; Development 121:4283-4291 (1995).

-i- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGI
                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).

-:- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

-:- DEVELOPMENTAL STAGE: FIRST DETECTED IN THE 10 H GASTRULA AROUND THE BLASTOPORE. IN LATER STAGES OF GASTRULATION AND EARLY NEURALIZATION, EXPRESSED IN POTERIOR MESODERM AND THE NOTOCHORD WHERE EXPRESSION CONTINUES AT LEAST UNTIL SWIMMING LARVAL STAGE.

-:- SIMILARITY: CONTAINS A T-BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Branchiostoma floridae (Florida lancelet) (Amphioxus)
Eukaryota; Metazoa; Chordata; Cephalochordata; Branch
PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS01283; TBOX_1; 1.
PFAM; PF00907; T-box; 1.
Developmental protein; Transcription regulation; DNA-binding;
Developmental protein; Multigene family.
                                                                                                               EMBL; X91903;
HSSP; P24781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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35, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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phioxus and vertebrates:
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                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Branchiostomidae;
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TAASPDQFSV SHLLSAVESE ISAGSEKGDP

GRRMFPVLKV

February 14, 2000 08:02

Type: P

TERDLKITLE

49253 MW;

T-BOX. ; 5948F2D3 CRC32;

DNHRWKYVNG

EWVPGGKPEP SVPSCVYIHP DSPNFGAHWM KSPVSFSKVK

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!!AA_SEQUENCE 1.0
ID BSR_BACCE STAN
ID BSR_BACCE
AC P33967;
DT 01-FEB-1994 (Rel. 2
DT 01-FEB-1994 (Rel. 2
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                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: MESODERM AND NOTOCHORD.
-!- SIMILARITY: CONTAINS A T-BOX DOMAIN.
HSSP: P24781; 1XBR.
HSSP: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96125169.

HOLLAND P.W.H., KOSCHORZ B., HOLLAND L.Z., HERRMANN B.G.; "Conservation of Brachyury (T) genes in amphioxus and ver developmental and evolutionary implications.";

Development 121:4283-4291(1995)

-:- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION REQUIRED FOR MESODERM FORMATION AND DIFFERENTIATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
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01-FEB-1996 (Rel. 33, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
BRACHYURY PROTEIN HOMOLOG 2 (AMBRA-2).
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Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                               STANDARD;
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28, Created)
28, Last sequence update)
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48469 MW; 4828EB28 CRC32;
                                                                                                                                                                                           PAPQTRITSN NWSPMTMPSM
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vertebrates:
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SQUERRE REPORTED TO SQUEET SQU

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Hydrolase; Zinc.
METAL 59
METAL 100
METAL 103
                                                                                                                                                                                                                                                                                                                                               **ROBAYASHI K., KAMAKURA T., TANAKA T., YAMAGUCHI I., ENDO T.;

**PNUCLEOCTIGE sequence of the bsr gene and N-terminal amino acid

sequence of blasticidin S deaminase from blasticidin S resistant

Escherichia coli TK121.";

Agric. Biol. Chem. 55:3155-3157(1991).

-!- FUNCTION: CATALYSES THE DEAMINATION OF THE CYTOSINE MOIETY OF THE

ANTIBIOTICS BLASTICIDIN S, CYTOMYCIN AND ACETYLBLASTICIDIN S.

-!- CATALYTIC ACTIVITY: BLASTICIDIN S + H(2)0 =

DEAMINOHYDROXYBLASTICIDIN S + NH(3).

-!- COFACTOR: ZINC (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES

-!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus cereus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                EMBL; S81409; AAC60404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K55-S1;
MEDLINE; 92144117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last annotation update) BLASTICIDIN-S DEAMINASE (EC 3.5.4.23).
                                                                                     PIR; JS0609; JS0609.
PROSITE; PS00903; CYT_DCMP_DEAMIN
PFAM; PF00383; dCMP_CYt_deam; 1.
                                                                                                                                                                                                                                                                                                                                      FAMILY
59 z
100 z
103 z
115573 ww;
                                                                                                             CYT_DCMP_DEAMINASES;
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f the bsr gene and N-terminal a
n S deaminase from blasticidin
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BSR_BACCE Length: 140 February 14, 2000 08:02 Type: P Check: 8425

ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
; 12D8CAEC CRC32;

SEQUENCE

140 AA;

- Н MKTFNISQQD LELVEVATEK ITMLYEDNKH HVGAAIRTKT GEIISAVHIE
- 51 AYIGRVTVCA EAIAIGSAVS NGQKDFDTIV AVRHPYSDEV DRSIRVVSPC
- 101 GMCRELISDY APDCFVLIEM NGKLVKTTIE ELIPLKYTRN

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_SEQUENCE 1.0

CAD1_DICDI

STANDARD; PRT; 213 AA.

P54657;

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-DCT-DEPENDENT CELL ADHESION MOLECULE-1 (DDCAD-1) (GP24).
                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 43-62 AND 118-133 MEDLINE; 96279194.
                                                                                                                          Dictyostelium discoideum (Slime mold).
Eukaryota; Dictyosteliida; Dictyostelium.
[]]
DEVELOPMENT
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IIAA_SEQUENCE 1.0

ICAMG_MOUSE
AC P49070;

AC P49070;

DT 01-FEB-1996 (R
DT 01-FEB-1996 (R
DT 01-FEB-1996 (R
DT 15-UIL-1998 (R
DT 15-UIL-1998 (R
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OC EURARYOTS; Met
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RN SEQUENCE FROM
RC STRAIN-B6/CBA,
RX MEDIANE; 96011
RA KIM H.S., MORE
RT CAICIUM SIGNA:
RT CLONING of ti
RT CAICIUM SIGNA:
RT Gene 163:323:-
CC -:- FUNCTION:
CC -:- SUBCELLUIL
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CC THIS SWISS-PR
CC EMBL; U21960;
DR MGD; MGI:1047
KW TRANSMEM TRANSMEM TRANSMEM
SSQ SEQUENCE 29
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SEQUENCE
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         Transmembrane.
TRANSMEM 188
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SEQUENCE 294 AA;
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Ol-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
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                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLUMBERG R.S.;

Cloning of the gene encoding the mouse homologue of the calcium signal-modulating ligand.";

Gene 163:333-324(1995).

Gene 163:333-324(1995).

FUNCTION: LIKELY INVOLVED IN THE MOBILIZATION OF CALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: LIKELY INVOLVED IN THE MOBILIZATION OF CALCIUM AS A RESULT OF THE TCR/CD3 COMPLEX INTERACTION. BINDS TO CYCLOPHILIN B.-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                                                                                                                       EMBL; U21960; AAA87004.1;
MGD; MGI:104728; CAML.
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(DB; DD02037; CADA.

adhesion; Calcium; Repeat.

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POTENTIAL.
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CAMG_MOUSE
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           EMBL; U18532; AAB59993.1; -...
EMBL; X17430; -; NOT_ANNOTATED_CDS.
EMBL; X217430; -; NOT_ANNOTATED_CDS.
EMBL; U29177; AAA70045.1; -..
EMBL; U29177; AAA70045.1; -..
EMBL; K02174; AAB05347.1; -..
EMBL; Z99116; CAB14459.1; -..
EMBL; Z9917; CAB14472.1; -..
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) (CDA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
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                                                                                                                                                                                                                                                                                                                     KIM K., HANG S., SUH J., SONG B.-H., HONG S., KIM J.;

"Nucleotide sequence upstream of the cdd locus in Bacillus subtilis.";

J. Microbid. Biotechnol. 5:0-0(1995)

-I. FUNCTION: THIS ENZYME SCAVENCE EXOGENOUS AND ENDOGENOUS CYTIDINE
-I. FUNCTION: THIS ENZYME SCAVENCE EXOGENOUS AND ENDOGENOUS CYTIDINE
-I. CATALYTIC ACTIVITY: CYTIDINE + H(2)0 = URIDINE + NH(3).

-I. COPACTOR: ZINC (BY SIMILARITY).

-I. SUBUNIT: HOMOTETRAMER.
-I. SUBUNIT: HOMOTETRAMER.
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Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a coperative of the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO SATO T., TAKECCHI M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SONG B.-H., NEUHARD J.;
"Chromosomal location, cloning and nucleotide sequence of the chromosomal location, cloning cytidine/deoxycytidine bacillus subtilis cdd gene encoding cytidine/deoxycytidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-168
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EMBL outstation -
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METAL 53
METAL 86
METAL 89
SEQUENCE 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BER; 93352438. THAM T.N., FERRIS S
                                                          CDSA_HAEIN
CDSA_HAEIN STANDARD; PRT; 288 AA P44937; 032623; 032627; 03262701-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma pirum.
Bacteria; Firmicutes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) (CDA).
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HSSP: P13652; 1AF2.
PROSITE: P800903; CYT_DCMP_DEAMINASES; 1.
Hydrolase; Zinc.
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PFAM; PF00383; dC
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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86 Z
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14854 MW;
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; F377B762 CRC32;
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PERENE ROOS GARAGA GARA
                                                                         CDSA_HAEIN
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Transmem 10
Transmem 52
Transmem 19
Transmem 152
Transmem 152
Transmem 152
Transmem 223
VARIANT 26
VARIANT 59
VARIANT 81
VARIANT 81
VARIANT 81
VARIANT 81
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EMBL; U60831;
EMBL; U60832;
TIGR; H10919;
PROSITE; PS013
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STRAIN-RD / KW20;

MEDLINE; 95350630,

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MEDLINE; 95350630,

MEDLINE; 95350630,

MERRICK J.M.,

MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCKYNE J.D.,

MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCKYNE J.D.,

SCOTT J.D., SHRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.E., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SNIH H.O.,

VENTER J.C.,

WENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ

-|- CATALYTIC ACTIVITY: CTP + PHOSPHATIDATE =

--- CDP-DIACYLGLYCEROL.

-|- PATHMAY: PHOSPHOLIPID BIOSYNTHESIS.

-|- PATHMAY: PHOSPHOLIPID BIOSYNTHESIS.
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PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.4) (CDP-DIGLYCERIDE
SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL
SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG
SYNTHASE).
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Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01315; CDS; 1. PFAM; PF01148; Cytidylylt Transferase; Nucleotidylt
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STRAIN-33;
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    MLKQRVLSAI VLIAAVLCAL
                                                                     Length:
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52
89
118
152
192
223
16
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59
81
288 AA;
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Nucleotidyltransferase;
e; Inner membrane.
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; AAB61967.1; -.
; AAB61972.1; -.
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                                                                 February
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FLFTPFYFAL
                                                                                                                                  POTENTIAL.

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PYROPHOSPHATE
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QPLIREFVTT FLGVFIFLWL YTEGNYLDAG
ALLLVISYPK SAKFWSKNPL LQLLFAFSTL

RVFEQHLQLL LINAVSWWGL

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YFSGRAFGKR KLAPKVSPGK SWEGVIGGLI

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CDSN_PIG
RP RP
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CDSN_PIG
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DOMAIN 155
DOMAIN 175
DOMAIN 175
DOMAIN 175
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01-MAR-1992 (Rel. 21,
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                  schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
schizosaccharomycetales; Schizosaccharomycetaceae;
schizosaccharomyces.
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itheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                 51
 SEQUENCE FROM N.A
                                                                                                                24865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scrofa (Pig).
arvota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBE outst European Bioinformatics Institute. There are no restrictions buropean Bioinformatics institute. There are no testrictions is non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: EXCUSIVELY EXPRESSED IN SKIN (BY SIMILARITY).
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21644 MW;
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MRI, outstation -
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ID CH19_DROGR
AC P13427;
DT 01-JAN-1990 (F
DT 01-JAN-1990 (F
DT 01-JCT-1996 (F
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Cell 66:149-159(1991)
Cell 60:149-159(1991)
Cell 60:149(1991)
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BUENO A., RÎCHARDSON H.E.,
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PIR; A40316; A40316
HSSP; P20248; 1JST
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PROSITE; PS00292; Cyclin; 1.
PFAM; PF00134; Cyclin; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
SEQUENCE 415 AA; 47827 MW; ED01A48C CR
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
CHORITON PROTEIN S19.
CP19 OR S19.
                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@ibrsib.ch).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE; 88297142.

MARTINED: CRUZADO J.C., SWIMMER C., FENERJIAN M.G., KAFATOS F.C.;

"Evolution of the autosomal chorion locus in Drosophila. I. General

"Evolution of the locus and sequence comparisons of genes s15 and
organization of the locus and sequence.";

Genetics 119:663-677(1988).
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Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Eukaryota: Neoptera: Endopterygota; Diptera; Brachycera: Musc
Ephydroidea: Drosophilidae: Drosophila.
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STRAIN-2.4.1;
MEDLINE; 95238260.
SCHILKE B.A., DONOHUE T.J.;
"ChrR positively regulates transcription of the Rhodobacter sphaeroides cytochrome c2 gene.";
J. Bacteriol. 177:1929-1937(1995).
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01-JAN-1988 (Rel. 01-JAN-1988 (Rel.
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: POSITIVELY REGULATES TRANSCRIPTION OF THE CYCA GENE FOR CYTOCHROME C2. MAY PLAY A ROLE IN THE INACTIVATION OF THE RPOE GENE.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
TRANSCRIPTIONAL ACTIVATOR CHRR.
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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COAT_TCV
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MEDLINE; 87112726.

HOGLE J.M., MAEDA A., HARRISON S.C.;
HOGLE J.M., MAEDA A., HARRISON S.C.;

"Structure and assembly of turnip crinkle virus. I. X-ray
"Structure and assembly analysis at 3.2-A resolution.";

J. Mol. Biol. 191:625-638(1986).

J. Mol. Biol. 191:625-638(1986).

J. Mol. Biol. 191:625-638(1986).

J. MOL. MARITY: COAT PROTEINS FROM CARMOVIRUSES (CARMV, MNSV, TCV),
DIANTHOVIRUSES (RCNMV), SOBEMOVIRUSES (MCMV, SBMV), TOMBUSVIRUSES
(AMCV, CNV, CYRSV, AND TBSV), AND TNV ARE RELATED IN THEIR S
                                                                                                                                                                                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE: 87283926.

STOCKLEY P.G., MORKIS T.J.;

"Structure and assembly of turnip crinkle virus. IV. Analysis of the coat protung gene and implications of the subunit primary structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssrn
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MEDLINE; 89243179.
CARRENGTON J.C., HEATON L.A., ZUIDEMA D., HILLMAN
"The genome structure of turnip crinkle virus.";
virology 170:219-225(1989).
351
                          301
                                                     251
                                                                                                                                        101
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PIR; S07285; S07285.
HSSP; P1195; ZIBV.
PROSITE; PS00555; ICOSAH_VIR_COAT_S; 1.
PFAM; PF00729; Viral_coat; 1.
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J. Mol. Biol. 194:265-276(1987).
[2]
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COAT PROTEIN.
                                                                                                                                                                                                                                                                                  DOMAIN
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239
252
351 AA;
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                          LGEAAAGSVQ
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                                                                                                                                        SEPGTFNQLI KEAAQYEKYR
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238 S
351 P
252 D
38052 MW;
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                                                                                                             NIEGCVSSVP
                                                                                                                                                                                             WOKKGWSTLT
                                                                                                                                                                                                                        14, 2000 08:02 Type:
                          WAGVKVAERG
                                                     TAGWEHDCHF
                                                                                                                                                                    TOPRVSTARD
                                                                               ANDAAQLGEV
                                                                                                                                                                                                                                                                 R DOMAIN, INTERACTION WITH S DOMAIN, VIRION SHELL. P DOMAIN, PROJECTING.
D -> Q (IN REF. 2).
                                                                                                                                                                                                                                                    -> Q (IN REF. 2).
064C2069 CRC32;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upda
21-JUL-1986 (Rel. 24, Last annotation up
01-DEC-1992 (Rel. 24, Last annotation up
COAT PROTEIN (P4 PROTEIN).
Tobacco streak virus (strain wC) (TSV).
Viruses; ssRNA positive-strand viruses,
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MEDLINE; 84169544.

CORNELISSEN B.J.C., JANSSEN H., ZUIDEMA D., BOL J.F.;

CORNELISSEN B.J.C., JANSSEN H., ZUIDEMA D., BOL J.F.;

Complete nucleotide sequence of tobacco streak virus

"Complete nucleotide sequence" (1984).
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P36562; P78075;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NICOTINATE.NUCLEOTIDE--DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE
(EC_2.4.2.21) (NN:DBI PRT) (N1-ALPHA-PHOSPHORIBOSYLTRANSFERASE).
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STRAIN-K12 / W3110;
MEDLINE 9606221B.
LAWRENCE J.G., ROTH J.R.;
"The cobalamin (coenzyme B12) biosynthetic coli.";
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIR-K12 / MG1655;

MEDLINE: 97426617.

BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYHEW G.F.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., GOEDEN M.A., ROSE D.J.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;

MAU B., SHAO Y.;
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                                 SEQUENCE FROM N.A.
STRAIN-K12;
                                                                                                                                                                                                         The
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                                                                                                                                                         complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-188 FROM N.A.

SEQUENCE OF 1-188 FROM N.A.

SETARINK12 / DH5-ALFRA;

COLLINS C. M., GUTMAN D.M., ISAZA J.;

COLLINS C. M., GUTMAN D.M., ISAZA J.;

COLLINS C. M., GUTMAN D.M., ISAZA J.;

SUBMILTED (XXX-1993) to the EMBL/GenBank/DDBJ databases.

SUBMILTED (XXX-1993) to the EMBL/GenBank/DDBJ databases.

I- PUNCTION: CATALYSES THE SYNTHESIS OF 5,6-DIMETHYLBENZIMIDAZOLE.

PHOSPHATE FROM NICOTINATE MONOUCLEDTIDE TO DMB.

PHOSPHATE FROM NICOTINATE NICOTINATE D-RIBONUCLEDTIDE +

CATALYTIC ACTIVITY: BETA-NICOTINATE D-RIBONUCLEDTIDE +

DIMETHYLBENZIMIDAZOLE.

-I- CATALYDLS COLMETHYLBENZIMIDAZOLE.

PATHWAY: COBALAMIN BIOSYNTHESIS, PART I AND III (COBII / COBII /

-I- PATHWAY: COBALAMIN BIOSYNTHESIS, PART II AND III (COBII / COBII /

-I- PATHWAY: COBALAMIN BIOSYNTHESIS, PART II AND III (COBII / COBII /

-I- PATHWAY: COBALAMIN BIOSYNTHESIS, PART II AND III (COBII / COBII /
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                                                                                                                                                                                  _SEQUENCE 1.0 STANDARD; PRT; 2
COX3_SCHCO STANDARD; PRT; 2
01-UAN-1990 (Rel. 13, Created)
01-EB-1999 (Rel. 33, Last sequence up
15-UUL-1999 (Rel. 38, Last annotation
CYTCCHROME C OXIDASE POLYPEPTIDE III (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U3333; AAA78908.1; --
EMBL; AB000291; AAC75052.1; --
EMBL; D90837; CAB21728.1; --
EMBL; D90838; CAB21739.1; --
EMBL; L25054; AAA56876.1; --
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CONFLICT 271
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Schizophyllum commune (Bracket fungus).
Mitochondrion.
Bukaryota; Fungi; Basidiomycota; Hymeno
Schizophyllaceae; Schizophyllum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTTSDLNS
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n biosynthesis; Porphyrin biosynthesis; Transferase;
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359 AA;
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301 L
; 36987 MW;
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-> V (IN REF. 1).
86515DE7 CRC32;
                                                    Hymenomycetes;
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ID COX4_SCHPO
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                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
EMBL; AB000399; BAA19097.1;
                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                         P79010;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
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                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1. CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
4 FERRICYTOCHROME C.

1. SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizophyllum commune.";
Curr. Genet. 14:401-403(1988).
C1- FUNCTION: SUBUNIT 1, II, AND III FORM THE FUNCTIONAL CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHELPS L.G., BURKE J.M., ULLRICH "Nucleotide base sequence of the
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SEQUENCE FROM N.A.
MEDLINE; 89106272.
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                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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25E315EF CRC32;
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mitochondrial COIII
                                                                                                                                                                                                                                                                                                                                                                                                                 164
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RRA RROCCOCCOCCATOR
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SEQUENCE FROM N.A., A
STRAIN=CV. PROGRESS N
MEDLINE; 91035597.
SCHNELL D.J., BLOBEL
"The chloroplast impo
                                                                                                                   (P36) (E30).

Pisum sativum (Garden pea).

Pisum sativum (Garden pea).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core_eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoid.
                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, CHLOROPLAST PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comp. b..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Exoskeletal proteins from the crab, Comp. Biochem. Physiol. 0:0-0(1999).
-!- TISSUE SPECIFICITY: CALCIFIED SHE STRUCTURAL PROTEIN: Cuticle; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CUTICLE PROTEIN CP1158 (CPCP1158)
Cancer pagurus (Rock crab).
Eukaryota, Metazoa, Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Cancroidea; Cancridae; Cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
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METAL
SEQUENCE
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TRANSIT 1
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PFAM; PF01215; CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSUE=CUTICLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAAAPAPPIP VSHYVASQQS VVGPSGIVSP SGNVQFSHEF ADNVVLVGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVGYSGIVSP DGNNIQFTHD FAHSIVLKGP SGIVTSDGKN LQLTAGQASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AA;
               BLOBEL G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
26
70
95
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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COX5B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion;
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11601 MW;
                                                         NO AND
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120
143
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                                                       9; TISSUE=SEEDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ion; Transit peptide; Zinc.
MITOCHONDRION (BY SIMILARITY).
CYTOCHROME C OXIDASE POLYPEPTIDE IV
ZINC (POTENTIAL).
ZINC (POTENTIAL).
ZINC (POTENTIAL).
MW; DA19B411 CRC32;
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CPTR_PEA
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"Molecular cloning and structural analysis of the phosphate
translocator from pea chloroplasts and its comparison to the spinach
phosphate translocator.";
planta 183:451-461(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chloroplast envelope contact sites.";
J. Cell Biol. 111:1825-1838(1990).
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modified and this statement is not remov
entities requires a license agreement (S
or send an email to licensedisb-sib.ch).
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EMBL; X68077; CAA48210.1; -..
PIR; S23774. S23774.
Transmembrane; Chloroplast; '
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LOCATED IN SUBCELLULAR EDUCATION: INTEGRAL MEMBRANE PROTEIN ENGRALE OF THE CHLOROPLAST.

SUBLITARITY: STRONG, TO OTHER PLANTS CIPT. ALSO SIMILAR TO YEAST PROTEIN SIX41.

CAUTION: WAS ORIGINALLY THOUGHT TO FUNCTION AS A CHLOROPLAST RECEPTOR.
                                                                                                                                                                                                           Length:
                                                                                                                                                                                    MESRVLSRAT TLSSLPTLNK LHRLPLANAS LPSVKSFGSV SDGGNLVWGR
                                                                                                                                                              QLRPELCSPV
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                       KRVFVIGFSI
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INTERMEMBRANE SPACE (POTENTIAL)
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                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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MBL outstation -
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!!AA_SEQUENCE 1.0
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01-FEB-1995
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOCKMANN J.;
Submitted (SEP-1994)
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01-FEB-1994 (Rel. 28, Last and
CYTOCHROME AA3 CONTROLLING PRO
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                                                                                                        Bacillus firmus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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MEDLINE; 93107080.

QUIRK P.G., HICKS D.B., KRULWICH T.A.;

Cloning of the cta operon from alkaliphilic Bacillus firmus characterization of the pH-regulated cytochrome caa3 oxidase encodes.";
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1995 (Rel. 31, Last sequence update)
1998 (Rel. 37, Last annotation update)
0PERON REPRESSOR (CSC OPERON REGULATORY
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STRAIN-168;

BERTERO M., PRESEGAN E., GLASER P., RICHOU A., DANCHIN A.;

SUBMITTED M., PRESEGAN E., GLASER P., RICHOU A., DANCHIN A.;

SUBMITTED M., CAUGH A.;

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                                   EMBL; M23915; AAA50254.1; -.
EMBL; Z98682; CAB11340.1; -.
EMBL; Z99111; CAB13360.1; -.
PIR; A33960; A33960.
SUBTILIST; BG10213; CTAA.
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Ol-JAN-1990 (Rel. 13, Last seq

15-JUL-1998 (Rel. 36, Last ann

CYTOCHROME AA3 CONTROLLING PRC
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MEDLINE; 89359135.

MUELLER J.P., TABER H.W.;

"Isolation and sequence of ctaA, a gene required foliosynthesis and sporulation in Bacillus subtilis.

J. Bacteriol. 171:4967-4978(1989).
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Bacteria; Firmicutes; Ba
Bactilus/Staphylococcus
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PIR; A45335; A45335.
Sporulation; Membrane.
SEQUENCE 297 AA; 32326 MW; BA198CC1 CRC32;
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-!- FUNCTION: CTAA IS REQUIRED FOR CYTOCHROME AA3 BIOSYNTHESIS AND INDEPENDENTLY FOR SPORULATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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us group; Bacillus.
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Sporulation; Membrane

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I I AA_SEQUENCE 1.0

ID CY2_RHOTE
AC P0098;
AC P0098;
DT 21-JUL-1986 (F
DT 21-JUL-1986 (F
DT 21-JUL-1995 (F
DT 21-JUL-1995 (F
DE CYTOCHROME C2.
OS Rhodcoyclus te
OC Bacteria; Prot
OC Rhodcoyclus te
OC Bacteria; Prot
OC Rhodcoyclus te
OC Bacteria; Prot
OC Rhodcoyclus te
OC RALON 3761;
RN [1]
RN SEQUENCE.
RL STRAIN-3761;
RY MEDLINE; 79195
RA AMBLER R.P., P
RT "Anomalies in
Cytochromes co;
RL Nature 278:661
CC -1-FUNCTION:
CC PHOTOSYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IIAA_SEQUENCE 1.0

ID CUU4_BLACR
AC P80675;
DI 15-JUL-1998 (F
DI 1
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SEQUENCE.

STRAIN-3761;
STRAIN-3761;
MEDLINE; 79199668.

AMBLER R.P., MEYER T.E., KAMEN M.D.;
AMBLER R.P., MEYER T.E., KAMEN M.D.;

"Anomalies in amino acid sequences of small cytochromes c and cytochromes c' from two species of purple photosynthetic bacteria.";

Nature 278:661-662(1979).

-!- EUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR, PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR TO THE OXIDIZED BACTERICHLOROPHYLL IN THE PHOTOHOSPHORYLATION PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTAA_BACSU Length: 306
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21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
01-NOV-1995 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 HAAISPLSVV SHPVVSPLVH VPQVVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhodocyclus tenuis (Rhodospirillum tenue).
Bacteria; Proteobacteria; beta subdivision; Rhodocyclus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT 31
REPEAT 84
SEQUENCE 127 AA;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL
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MEDLINE; 97218697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
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JENSEN U.G., ROTHMANN A., SKOU L., ANDERSEN S.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cuticular proteins from the giant cockroach, Insect Biochem. Mol. Biol. 27:109-120(1997). Structural protein; Cuticle; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAVLYPSIYS ILSKSKVRVQ ELEPVEGAAV PADTKKAEIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLIFITLQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01, Created)
01, Last sequence update)
32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVFGSNALIM ALHFGISLIS FASVLILTLL
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2.
4W; 26A82D7C CRC32;
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II JAA_SEQUENCE 1.0
IID CYNR_ECOLI
AC P27111;
AC P2711;
AC P
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METAL
SEQUENCE
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BINDING
BINDING
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PROSITE; PS00190; (
PFAM; PF00034; CYTC
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HSSP; P00
PROSITE;
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01-AUG-1992 (Rel. 23, Last
01-NOV-1997 (Rel. 35, Last
CYN OPERON TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE; 97426617.

BLACTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V BLACTNER F.R., PLUNKETT G. F., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE D.J., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92276346.

SUNG Y.-C., FUCHS J.A.;

"The Escherichia coli K-12 cyn opmember of the lysk family.";

J. Bacteriol. 174:3645-3650(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation. The European Bioinformatics Institute. There are no restrictions on its table by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       The complete genome sequence of Escherichia Science 277:1453-1474(1997).
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  EMBL; M93053; AAA23628.1;
EMBL; AE000141; AAC73441.1
EMBL; U73857; AAB18062.1;
PIR; A41900; A41900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.
SIMILARITY: THIS SEQUENCE IS MORE CLOSELY RELATED TO THE SEQUENC
OF CYTOCHROME C551 FROM PSEUDOMONAS AND AZOTOBACTER THAN TO THE
SEQUENCES OF CYTOCHROME C2 FROM OTHER SPECIES OF RHODOSPIRILLUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGQGVWAKQL GAEIPMPANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADESALAQTK GCLACHNPEK
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                                                                                                                                                                                                                                                                                     REGULATORS.
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12
15
16
66
66
92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; cytochrome_c; 1.
sport; photosynthesis; H
HEME (CO)
15 15 HEME (CO)
15 16 IRON (HE)
16 16 IRON (HE)
16 66 66 IRON (HE)
2 AA; 9781 MW; 573C3CFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCQF2T
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IRON (HEM
IRON (HEM
573C3CF0
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E (COVALENT).
E (COVALENT).
N (HEME AXIAL LIGAND).
N (HEME AXIAL LIGAND).
C3CF0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision;
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TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 30-85, AND ACTIVE SITE.

SEQUENCE OF 30-85, AND ACTIVE SITE.

WEDLINE: 89350853.

A LEYH-BOUILLE M., VAN BEEUMEN J., M.;

A LEYH-BOUILLE M., GHUYSEN J.-M.;

ANGUYEN-DISTECHE M., GALLAN J.-M.;

ANGUYEN-DISTECHE M., GALLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECOGENE: EG11421; CYNR.

PROSITE: PS00044; HTH_LYSR_FAMILY:
PFAM; PF00116; HTH_1; 1.
Transcription regulation; DNA-bind:
18 37 H-T-H
DNA_BIND 18 37 H-T-H
SEQUENCE 299 AA; 32961 MW; 0A8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p39042;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
D-ALMNYLD-ALMNING CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.4) (DD-PEPTIDASE) (DD-CARBOXYPEPTIDASE).
Streptomyces sp. (strain K15).
Streptomyces sp. (strain K15).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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DACX_STRSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALOMEQUE MESSIA P., ENGLEBERT S., LEYH-BOUILLE M.,
MGUYEN-DISTECHE M., DUEZ C., HOUBA S., DIDEBERG O.,
VAN BEBUMEN J., GHUYSEN J.-M.;
"Amino acid sequence of the penicillin-binding protein/DD-peptidase
"Amino acid sequence of the penicillin-binding protein/DD-peptidase
of Streptomyces K15. Predicted secondary structures of the low Mr
penicillin-binding proteins of class A.";
Biochem. J. 279:223-230(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 92028812.
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                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.ch).
                                                                                                        EMBL; X59965; CAA42591.1; -.
PIR; S04638; S04638.
PIR; S17674; S17674.
PFAM; PF00768; Peptidase_S11;
Hydrolase; Carboxypeptidase: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKAISLAPPL LERTAVLLRR KNSWQTAAAK
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H-T-H MOTIF (BY SIM
MW; 0A8298D6 CRC32;
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                                                                                                                    Peptidoglycan
                D-ALANYL-D-ALANINE
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                            CARBOXYPEPTIDASE
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or send an ema...

R EMBL; U28135; AAB01679.1; -...

R EMBL; U28135; CAA99237.1; -...

DR EMBL; Z74954; CAA99237.1; -...

DR EMBL; Z74955; CAA99239.1; -...

DR PIR; D34848; D34848

BR SGD; L000329; DBED, ATP_HELICASE; 1.

PROSITE; PS00039; DEAD, TP_HELICASE; 1.

DR PFAM; PF00271; helicase_C; 1.

DR PFAM; PF00271; helicase_C; 1.

RW Helicase, ATP-binding; RNA-binding; Nuclear protein.

NP_BIND 138 145

NP_BIND 239 242

DEAD BOX.

TAR74 MW; C70FB665 CRC32;
                                                                         REPUBLINE; 90160368.

RA MEDILINE; 90160368.

RA CHANG T. -H., ARENAS J., ABELSON J.;

RA CHANG T. -H. ARENAS J., ABELSON J.;

RA CHANG T. -H., ARENAS J., ABELSON J.;

RA CHANG T. -H., ARENAS J., ABELSON J.;

RA CHANG T. -H., ARENAS J., ABELSON J.;

RA PICC. NAIL ACAD. SCI. U.S. A. 87:1571-1575(1990).

C. -- SURGELULIAR IOCATION: NUCLEAR (PROBABLE).

C. -- SURGELLULIAR IOCATION: NUCLEAR (PROBABLE).

C. -- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.

C. -- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.

C. -- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.

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C. -- SIMILARITY: TO OTHER "DEAD" BOX FAMILY HELICASES.

C. -- SIMILARITY: TO OTHER TO BOX FAMILY HELICASES.

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LANDT O., HIESEL R., UNSELD M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBP5_YEAST STANDARD; PRT; 482 AA.
P20449;
01-FEB-1991 (Rel. 17, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. CHANG T.-H.;
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CONFLICT
CONFLICT
SEQUENCE
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SOHN C., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER B., DANG D.V.,
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70
83
291 AA;
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30257 MW;
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T -> Q (IN REF. 2).
D -> S (IN REF. 2).
; E2D9DFE9 CRC32;
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i (AA_SEQUENCE 1.0 ID DHAT_CITER STANDARD, AC P455.13; DT 01-NOV-1995 (Rel. 32, Created)

101

DNIVTSVALA

51

VLSKNPVYSN VMKEDDPQVI NHIALAKQAD LFLLPPASAN TLAHLAHGFA

LSHQLTKLGY HVNVFMTNAA KQFIPPLTLQ

Check: 9135

LPLEVPKFFA PAMNTKMYEN PITQSNITLL KKFGY

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MTKKILLAVS GSIAAYKAAD

DFP_STRMU Length: 145 February 14, 2000 08:02 Type: P

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I!AA_SEQUENCE 1.0

ID DFP_STRMU
AC Q54433;
DT 01-NOV-1997 (F
RT STRAIN-NG8;
RX SEQUENCE FROM
RC STRAIN-NG8;
RX SEQUENCE FROM
RC STRAIN-NG8;
RX SEQUENCE FROM
RC STRAIN-NG8;
RX ST
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                  Flavoprotein.
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14
SEQUENCE 145
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GUTIERREZ J.A., CROMLEY P.J., BROWN D.P., HILLMAN J.D.,

GUTIERREZ J.A., CROMLEY A.S.;

"INSERTIONAL P., BLEIWEIS A.S.;

"Insertional mutagenesis and recovery of interrupted genes of
Streptococcus mutans by using transposon Tn917: preliminary
characterization of mutants displaying acid sensitivity and
utritional requirements.";

or provided the provided transposon transposon transposon transposon

mutritional requirements.";

1. FUNCTION: FLAVOPROTEIN AFFECTING SYNTHESIS OF DNA AND PANTOTHENATE

METABOLISM (BY SIMILARITY).
                                                                                                                                       EMBL; U48885; AAC44502.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG (FRAGMENT).
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145 AA;
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15819 MW; 24E84944 CRC32;
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DHAT_CITER Length:
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01-NOV-1997 (Rel. 35, Last annotation update)
1,3-PROPANEDIOL DEHYDROGENASE (EC 1.1.1.202) (3-HYDROXYPROPIONALDEHYDE
REDUCTASE) (1,3-PROPANEDIOL OXIDOREDUCTASE).
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BOANIEL R., BOENIGK R., GOTTSCHALK G.;

"purtification of 1,3-propanediol dehydrogenase from Citrobacter

"purtification of 1,3-propanediol dehydrogenase from Citrobacter

freundii and cloning, sequencing, and overexpression of the

corresponding gene in Escherichia coll.";

J. Bacteriol. 177:2151-2156(1995).

J. Bacteriol. 177:2156(1995).

J. Bacteriol. 177:2156(199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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PROSITE; PS00913; ADH_IRON_1; 1.

PROSITE; PS00060; ADH_IRON_2; 1.

PFAM; PF00465; Fe-ADH; 1.

Oxidoreductase; NAD; Iron.
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                                                                                _SEQUENCE 1.0

DHAT_KLEPN STANDARD; PRT; 387 AA.
Q59477;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
Q1-NOV-1997 (Rel. 35, Last annotation update)
1,3-PROPAMEDIOL DEHYDROGENASE (EC 1.1.1.202)
1,3-PROPAMEDIOL DEHYDROGENASE (EC 1.1.1.202)
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                                             Klebsiella
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CATALYTIC ACTIVITY: PROPANE-1,3-DIOL + NAD(+) =
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SIMILARITY: BELONGS TO THE
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Proteobacteria;
                           Proteobacteria;
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                                               pneumoniae
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41481 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVVGERCKL
                                                                                                                                                                                                                                                                                                                                                                          HQLGGLYDMP
                                                                                                                                                                                                                                                                                                                                 MDAAELAIHA
                                                                                                                                                                                                                                                                                                                                                                                                                  IQAIRLIARN
                                                                                                                                                                                                                                                                                         PRKGNEKEIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC88846 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000
                                subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGKKALLVT DKGLRAIKDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRDGLEVFRK
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                                                                                                                                                                                                                                                                                                                                 IARLSADIGI
                                                                                                                                                                                                                                                                                       EIFRQAF
                                                                                                                                                                                                                                                                                                                                                                            HGVANAVLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type: P
                                                                                                                      (3-HYDROXYPROPIONALDEHYDE
                                   Enterobacteriaceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHCDIIVTVG
                                                                                                                                                                                                                                                                                                                                                                                                                         LKARENMAYA
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                                                                                                                                                                                                                                                                                                                                                                                 HVARYNLIAN
                                                                                                                                                                                                                                                                                                                                      PQHLRDLGVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Check:
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DHAT_KLEPN Length:
PT RAY AND RAY
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STRAIN-ATCC 25955;
STRAIN-ATCC 25955;
STRAIN F.A., WILLARD B.L., CAMERON D.C.;
SKRALY F.A., WILLARD B.L., CAMERON D.C.;
SUBMITTED (NOV-1995) to the EMBL/GenBank/DDBJ data submitted (NOV-1995) to the EMBL/GenBank-DJ (NOV-1995) to the EMBL/GENBAR (NOV-1995) to the EMBL/GENBAR (NOV-1995) to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation is the European Bioinformatics Institute. There are no restrictions on its table modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DHB3_HUMAN
P37058:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U30903; AAA74260.1; -.
PROSITE; P800913; ADH_IRON_2; 1.
PROSITE; P800060; ADH_IRON_2; 1.
PFAM; PF00465; Fe_ADH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ox1doreductase; SEQUENCE 387
VARIANT MPH TRP-80.
WEDLINE; 98429412.
BILBAO JR., LORIDAN L., A
BILBAO JR., LORIDAN L., A
novel missense (R80W) m
dehydrogenase type 3 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (
TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE)
HSD1783 OR EDH1783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=TESTIS; /
MEDLINE; 94355972.
GEISSLER W.M., DAVI
MENDONCA B.B., ELLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Н
                                                                                                                                                                                                                                                                                       Male pseudohermaphroditism causeontain pseudohermaphroditism causeontain participation with the market production and the 
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SUBUNIT: HOMOOCTAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IRON-CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVDKTLHYLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             DAVIS D.L., WU ELLISTON K.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKVKFVIVSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND VARIANTS MPH Q-80; V-203;
         AUDI L., GONZALO E., CASTANO L.;
mutation in 17-beta-hydroxysteroi
e associated with male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISVVGERCQL LGGKKALLVT DKGLRAIKDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  L., BRADSHAW WILSON J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000
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D(+) = 3-HYDROXYPROPANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQARENMAYA
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                                                                                                                                                                                                                                                                                                                                                    of testicular
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LL D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-232
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gene

pseudohermaphroditism.";
Eur. J. Endocrinol. 139:330-333(1998).
1- FUNCTION: FAVORS THE REDUCTION OF ANDROSTENEDIONE TO TESTOSTERONE.
USES NADPH WHILE THE TWO OTHERS EDH1/B ENZYMES USE NADH.
-!- CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NADP(+) = ESTRONE +

NADPH.

PATHWAY: LAST ENZYME OF THE TESTOSTERONE BIOSYNTHESIS.

DISEASE: DEFECTS IN EDH17B3 GIVE RISE TO MALE PSEUDOHERMAPHRODISM (MPH): THESE 46,XY INDIVIDUALS HAVE UNAMBIGUOUS EMMALE EXTERNAL GENITALIA AT BIRTH, BUT FAIL TO MENSTRUATE AT THE TIME OF EXPECTED PUBERTY AND INSTEAD VIRILISE AS EVIDENCED BY GROWTH OF THE PHALLUS, BREAST DEVELOPMENT MAY OR MAY NOT TAKE PLACE.

SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.

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ID DHB3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHB3_HUMAN Length: 310 February 14, 2000
                                                                                   P703E5;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (1:
(TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
HSD17B3 OR EDH17B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steroid biosynthese, Desendohermaphroditism, Desendohe
                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                          201
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MIN; 204300; -
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
Steroid blosynthesis; Oxidoreductase; NADP; Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
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                                               Mammalia;
Mus.
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+ +
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EYRDKGIIIQ VLTPYSISTP MTKYLNNKMT KTADEFVKES

RRKGLILNIS

SGAALRPWPL

YSLYSASKAF SSSGESQNLI TTGSGVKIVQ MRFSQHLFLR FCKALPSSFL RSMGQWAVIT

Check:

CGCLAHEIIA

IILNRIPSRI

FYSSTAQRFL LTRYSDYLKR

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DHB3_MOUSE Length: 305 February 14, 2000 08:02 Type: P
                                          PFAM; PFO
Steroid b
NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                      EMBL; U668
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
MEDLINE; 97325842.
SHA J.A., DUDLEY K., RAJAPAKSHA W.R.A., O'SHAUGHNESSY P.J.;
Sequence of mouse 17beta-hydroxysteroid dehydrogenase type 3 cDNA
and tissue distribution of the type 1 and type 3 isoform mRNAs.";
J. Steroid Biochem. Mol. Biol. 60:19-24(1997)
-1- FUNCTION: FAVORS THE REDUCTION OF ANDROSTENEDIONE TO TESTOSTERONE.
USES NADPH WHILE THE TWO OTHERS EDH17B ENZYMES USE NADH (BY
                                                                                                                                                                                                                                                                                                                                        ----
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                                                                                                                                                                                                                                                                            SIMILARITY).

CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NADP(+) = ESTRONE + NADPH.

NADPH.

PATHWAY: LAST ENZYME OF THE TESTOSTERONE BIOSYNTHESIS.

SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.
                                                                                      TE; PS00061; ADH_SHORT; 1.
PF00106; adh_short; 1.
id biosynthesis; Oxidoreduc
                                                                                                                                          U66827; AAB06793.1; -.
MGI:107177; HSD17B3.
                                          194
305 AA;
                                  BY SIMILARITY.
34271 MW; 10CB2855 CRC32;
                                                               Oxidoreductase; NADP; Multigene NADP (BY SIMILARITY).
                                                                                                                                                                                          moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                           a collaboration
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ID DHB3_RAT
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
ESTRADIOL 17 BETA-DEHYDROCENASE 3 (EC 1. 1. 62) (17-
(TESTICULAR 17-BETA-HYDROXYSTEROID DEHYDROGENASE).
HSD17B3 OR EDH17B3.
Rattus norvegicus (Rat).
Rutaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                         SEQUENCE FROM N.A.

KHANUM A., TSAI-MORRIS C.-H., DUFAU M.L.;
SUBMILTED (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FAVORS THE REDUCTION OF ANDROSTENEDIONE TO TES
-!- CUSES NADEH WHILE THE TWO OTHERS EDH17B ENZYMES USE NADH
SIMILARITY).
-!- CATALYTIC ACTIVITY: ESTRADIOL-17-BETA + NADP(+) = ESTRON
NADPH.

NADPH:

PATHWAY: LAST ENZYME OF THE SIMILARITY: BELONGS TO THE SEMILARITY: BELONGS TO THE SEMILARITY (SDR). 17-BETA-HSD 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                 THE TESTOSTERONE
                                    SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                                              BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                               (17-BETA-HSD
                                                                                                                                                                                                                                                                                                          Mammalia;
Rattus.
                                                                                                              ESTRONE
                                                                                                                                                                             TESTOSTERONE
                                                                                                                                                            (BY
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RRN OCC OCC

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DHB3_RAT
                                 !!AA_SEQUENCE 1.0
ID DHBK_MOUSE
DHBK_MOUSE
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SEQUENCE
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NP_BIND
ACT_SITE
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PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
PFAM; PF00106; adh_Short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
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                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C; TISSUE-LIVER;
STRAIN-BALB/C; TISSUE-LIVER;
GAMBOTTO A., PAGLIANO O., ROBBINS P., DELEO A.;
GAMBOTTO A., PAGLIANO O. TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
SUBMILTED BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
-!- SIMILARITY: BELONGS TO THE SHORT-CHAILY.
FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.

FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
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15-DEC-1998 (Rel. 37, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
15-JUL-1999 (Rel. 38, Last annotation
putarive STEROID DEHYDROGENASE KIK-I o
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMEL outstake European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute. There are no restrictions as by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                    EMBL; AF064635; AAC16885.1; -. PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                             NP_BIND
                                                                                                     Steroid
                                                                                                                        PFAM; PF00106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 306 February 14, 2000 08:02 Type: P
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NADP (BY SIMILARITY)
194
194
BY SIMILARITY
194
BY BFB8CBB9 CRC32;
  Length: 312
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306 AA;
                                                                                                biosynthesis;
                                        50
202
312 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYRDKGIIIQ
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                                                                                                                        adh_short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus
                                            202
34742 MW;
       February 14, 2000 08:02
                                          Oxidoreductase; NADP; Multigene family.

NADP (BY SIMILARITY).

BY SIMILARITY.

12 BY SIMILARITY.

14742 MW; 121C2554 CRC32;
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(EC 1.1.1.-).
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                Type:
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MECAPPAAGE LYWVGASTIA YLALRASYSL FRAFQVWCVG NEALVGPRLG

AKRGMKIVLI SRSQDKLNQV SNNIKEKFNV

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!!AA_SEQUENCE 1.0
| | AA_SEQUENCE 1.0

ID DHC3_HUMAN

AC 075828;

DT 15-DEC-1998 ()

DT 15-DEC-1999 ()

DT 15-DEC-1999 ()

DE CARBONYL REDU

DE CARBONYL REDU

DE REDUCTASE 3).

GN CBR3.

GN CBR3.

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O57314;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last sequence update)
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SUBMITTED (NOV-1997) to the EMBL/GenBank/DDBJ databases.

-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
--- FAMILY (SDR). 17-BETA-HSD 3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way non-different is not removed. Usage by and for commercial modified and this statement is not removed. Usage by shock/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                   075828;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
CARBONYL REDUCTASE [NADPH] 3 (EC 1.11.1.184) (
  Homo sapiens (Human)
Eukaryota; Metazoa; (
Eutheria; Primates; )
                                                                                                                                                                                                                                                                                                                                   301
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                                                                                                       REDUCTASE 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biosynthesis; Oxidoreductase; NADP; Multigene 48 77 NADP (BY SIMILARITY).

E 201 201 BY SIMILARITY.

E 312 AA; 33896 MW; 3DDB3A6D CRC32;
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              Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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DHC3_HUMAN
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P16152;
01-APR-1990 (Rel. 14, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
CARBONYL REDUCTASE [NADPH] 1 (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE) (PROSTAGLANDIN-E2 9-REDUCTASE) (EC 1.1.1.189)

(PROSTAGLANDIN 9-KETOREDUCTASE) (15-HYDROXYPROSTAGLANDIN DEHYDROGENASE (NADP+1) (EC 1.1.1.197).

CBR1 OR CBR OR CRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
NP_BIND
ACT_SITE
SEQUENCE
                                                           WERMOTH B., BOHREN K.M., HEINEMANN G., VON WARTBURG J.-P., GABBAX K.H.;

"Human carbonyl reductase. Nucleotide sequence analysis of a cDNA amino acid sequence of the encoded protein.";

J. Biol. Chem. 263:16185-16188(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB004854; BAA33500.1;
EMBL; AB003151; BAA34207.1;
MIM; 603608; -
PROSITE; PS00061; ADH_SHORT;
PFAM; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the Exponent Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 98414514.
WATANABE K., SUGAWARA C., ONO A., FUKUZUMI Y., ITAKURA S.,
YAMAZAKI M., TASHIRO H., OSOGGAWA K., SOEDA E., NOMURA T.;
YAMAZAKI M., TASHIRO H., OSOGGAWA K., SOEDA E., NOMURA T.;
PAMAZORI M., TASHIRO H., OSOGGAWA K., SOEDA E., NOMURA T.;
PSEUDOGGENES to human chromosome 21q22.2.";
PSEUDOGGENES TO HUMAN CHOPLEY F. CORTALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                             SEQUENCE FROM N.A.,
                                                                                                                                                        TISSUE-PLACENTA;
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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NADP (BY SIMILARITY).
BY SIMILARITY.
; AE7D716B CRC32;
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EMBL; J04056; AAA52070.1; -.
EMBL; M62420; AAA17881.1; -.
EMBL; AB003151; BAA33498.1; -.
PIR; A31912; RDHUCB.
PIR; A31912; RDHUCB.
PIR; S09013; S09013
HSSP; P11061; IFDW.
MIM; 114830; -.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
Oxidoreductase; NADP; A
INIT_MET 0 0
MOD_RES 1 1 1
MOD_RES 238 238
MOD_RES 238 238
NP_BIND 9 3
ACT_SITE 193 193
SEQUENCE 276 AA; 302
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 92017676.
FOREST G.L., AKMAN S., DOROSHOW J., RIVERA H., KAPLAN W.D.;
FOREST G.L., AKMAN S., DOROSHOW J., RIVERA H., KAPLAN W.D.;
"Genomic sequence and expression of a cloned human carbonyl reductase
gene with daunorubicin reductase activity.";
"~1 pharmacol. 40:502-507(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.

MEDILINE; 9313816.

KROOK M., GHOSH D., STROEMBERG R., CARLQUIST M., JOERNVALL H.:

"Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-

Proc. Natl. Acad. Sci. U.S. A. 90:502-506(1993)

-!- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL COMPOUNDS INCLUDING THE ANTITUMON FANTHRACYCLINE ANTIBLOTICS.

CAN CONVERT PROSTAGLANDIN E2 TO PROSTAGLANDIN E2-ALPHA.

-!- CATALYTIC ACTIVITY: R-CHOH-R' + NADPH+) - R-CO-R' + NADPH-

-!- CATALYTIC ACTIVITY: (5Z.13E)-(15S)-9,11,15-TRIHYDROXYPROSTA-5,13-

DIENOATE + NADPH.

- STATUTTY NOTHER (5Z.13E)-(15S)-11,15-DIHYDROXYPOSTA-5,13-

DIENOATE + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDITINE; 98414514.

WATANABE K., SUGAWARA C., ONO A., FUKUZUMI Y., ITAKURA WATANABE K., SUGAWARA C., ONO B., FUKUZUMI Y., ITAKURA PAMAPAKI M., TASHIRO H., OSOBGAWA K., SOEDA E., NOMURA "Mapping of a novel human carbonyl reductase, CBR3, and pseudogenes to human chromosome 21q22.2.";

Genomics 52:95-100(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORREST G.L., AKMAN S., KRUTZIK S., PAXTON R.J., SPARKES R.S., DOROSHOW J., FELSTED R.L., MOHANDAS T., BACHUR N.R.;
"Induction of a human carbonyl reductase gene located on chromosome 21.";
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is p between the Swiss Institute of Bioinformate the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,13-DIENOATE + NADPH.

CAPALTYTC ACTIVITY: (5Z,13E)-(15S)-11-ALPHA,15-DIHYDROXY-9-
OXOPROST-13-ENOATE + NADPY+) = (5Z,13E)-11-ALPHA-HYDROXY-9,15-
DIOXOPROST-13-ENOATE + NADPH.
SUBUNTY: MONOMER.
SUBUNTY: MONOMER.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
                                                                                                                   Acetylation.
      ¥
ACETYLATION.
N6-(1-CARBOXYETHYL).
NADP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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DHCA_HUMAN ы Length: 276 February 14, 2000 08:02 P Check: 3202

SSGIHVALVT GGNKGIGLAI VRDLCRLFSG DVVLTARDVT RGQAAVQQLQ

AEGLSPREHQ LDIDDLQSIR ALRDFLRKEY GGLDVLVNNA GIAFKVADPT

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ED DE FED
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                                                                                                                                                                                                                                                              EMBL; U31966; AAB19006.1; -.

MGD; MGI:88264; CBR.

PROSITE; PSO0061; ADH_SHORT; 1.

PRAM; PF00106; adh_short; 1.

Oxidoreductase; NADP; Acetylation
OXIDORES
INIT_MET

NP_BIND
ACT_SITE
193
SEQUENCE
276 AA; 30597 MW; 09
__SEQUENCE 1.0
DHCA_RABIT
P47844;
01-FEB-1996 (
01-FEB-1996 (
15-DEC-1998 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            murine genes that express cbr map
Genomics 34:147-148(1996).
-!- CATALYTIC ACTIVITY: R-CHOH-R'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBR OR CBRI.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutharia; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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"Cloning a cDNA for carbonyl reductase (Cbr) from mouse cerebellum:
murine genes that express cbr map to chromosomes 16 and 11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL
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P48758;
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WEI J., DLOUHY S.
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                                                                                                                                        TITEEELVGL MNKFVEDTKK
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37,
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P; Acetylation.

O BY SIMILARITY.

1 ACETYLATION (BY SIMILARITY).

13 NADP (BY SIMILARITY).

193 BY SIMILARITY.

193 BY SIMILARITY.

30597 MW; 09438E74 CRC32;
                                                                                                                                                                                                                                       February 14, 2000 08:02 Type: P Check:
Created)
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                                                                                                                                                                                                                  TRDLCRKFSG
                                                                                       KKVEPW
                                                                                                              LINACCPGWV
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Mus.
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DHCA_RABIT
                                        This SWISS-PROT entry is copyright. It is produced through a coll:

C between the Swiss Institute of Bioinformatics and the EMBL out:

C the European Bioinformatics Institute. There are no restriction:

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C modified and this statement is not removed. Usage by and for or

C entities requires a license agreement (See http://www.isb-sib.ch/

C or send an email to license@isb-sib.ch).

C EMBL; U07051; AAA77670.1;

R EMBL; U09244; AAA88119.1;

R PROSITE; PS00061; ADH_SHORT; 1.

R PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95197021.
GONZALES B., SAPRA A., RI
"Cloning and expression of
reductase.";
Gene 154:297-298(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lágomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE).
                                      SEQUENCE
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Length: 276
                                  214
276 AA;
February 14, 2000
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n of the cDNA
                                        MW.
                                BY SIMILARITY.

NADP (BY SIMILARITY).

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A -> E (IN CLONE RCBR6;
V -> A (IN CLONE RCBR6
V -> A (IN CLONE RCBR6
H -> Q (IN CLONE RCBR6
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NA encoding rabbit
    08:02
Type: P
                                                   RCBR6).
RCBR6).
RCBR6).
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t liver carbonyl
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IIAA_SEQUENCE 1.0

DHCA_RAI

AC P44727;

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Last sequence update)
DT 01-CCT-996 (Rel. 34, Last annotation update)
DE CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL DE REDUCTASE)
DE REDUCTASE).
OC RRUCTASE).
OC BR.
CBR.
OS Rattus norvegicus (Rat).
OC ENKaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
CC Eukaryota; Redentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
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TITEEELVGL

LSEHRGGDKI

DVLLTAQDEA
GGLNVLVNNA
GGRVVNVSSM
GVHQTEGWPD
RTDMGGPNAT

TAYGVTKMGV

PELQQKFRSE TVLSRIQARH VYLALLPPDA

EGPHGQFVMD

TRALCRLESG
ALRDFLRRAY
CTELLPLMRP
MKKFVEDTKK
LVNACCPGWV
KKVEQW

51

AEGLSPRFHQ

GANKGVGFAI LDITDLQSIR

VIAFKMEDTI

KINFDGIRDV

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DHCA_RAT
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DHK1_STRVN
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                                                                                                                                                                                                                                                                  (EC 13117) (ORF3).
Streptomyces violaceoruber.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
GRANATICIN POLYKETIDE SYNTHASE PUTATIVE KETOACYL
                                                                                                                                      "Structure and deduced function of the granaticin-producing polyketide synthase gene cluster of Streptomyces violaceoruber Tu22.";
                                                                                                                                                                                 MEDLINE; 90060034.
SHERMAN D.H., MALPARTIDA F.,
HOPWOOD D.A.;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=TU22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Eur. J. Biochem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS;
MEDLINE; 95220378.
MERMUTH B., MAEDER-HEINEMANN G., ERNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oning and expression of carbonyl reductase from rat testis.";
J. Biochem. 228:473-479(1995).
CARALYIIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCLLULAR LOCATION: CYTOPLASMIC.
SYMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
European
by non
                                                                      OJ. 8:2717-2725(1989).
PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC GRANATICIN.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its
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276 AA;
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30447 MW;
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ACETYLATION (BY SIMILARITY).

NADP (BY SIMILARITY).

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SIMILARITY

O447 MW; D9BC158B CRC32;
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EMBL; Z11511; CAA77599.1;
BIR; S25079; S25079.
HSSP; P19992; ZHSD.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
PFAM; PF00678; adh_short; 2.
Antibiotic biosynthesis; Oxidoreductase; NAD.
AND_BIND 10 NAD (BY SIMILARITY)
ACT_SITE 157 157 BY SIMILARITY.
SEQUENCE 261 AA; 27080 MW; 12DFE5B3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITATE 2374944.

MEDITATE 2374944.

ARROWSMITH T.J., MALPARTIDA F., SHERMAN D.H., BIRCH A., HOPWOUL L.A., ARROWSMITH T.J., MALPARTIDA F., SHERMAN D.H., BIRCH A., HOPWOUL L.A., ROBINSON J.A.;

"Characterisation of acti-homologous DNA encoding polyketide synthase "Characterisation";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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PFAM; PF00106; adh_Short; 1.
PFAM; PF00678; adh_Short_C2; 1.
Antiblotic biosynthesis; Oxidoreductase; NAD.
NP_BIND 1 45 NAD (BY SIMILARITY).
RCT_SITE 168 168 BY SIMILARITY.
SEQUENCE 272 AA; 28393 MW; 1C3C79A3 CRC32;
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EMBL;
PIR; (
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01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
01-CCT-1996 (Rel. 34, Last annotation update)
MONBONSIN POLYKETIDE SYNTHASE PUTATIVE KETOACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from the monensin producer Streptomyces cinnamonensis.";
MO1. Gen. Genet. 234:254-264(1992).
-i- PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC MONENCIN.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
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X16144; CAA34263.1; -.

S05397; S05397.

; P03617; LIFK.
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MBL outstation -
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IIAA_SEQUENCE 1.0

ID DITE_BACSU
AC P39577;
DT 01-FEB-1995 (
DT 01-FEB-199
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                                    DLTE_BACSU
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01-FEB-1995 (Rel. 34, Las
01-OCT-1996 (Rel. 34, Las
DLTE PROTEIN.
DLTE OR IPA-IR.
Bacillus subtilis.
Bacteria; Firmicutes; Bac
Bacillus/Staphylococcus 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Incorporation of D-alanine into lipoteichoic acid and wall teichoic acid in Bacillus subtilis. Identification of genes and regulation.";
J. Biol. Chem. 270:15598-15606(1995).
I- PATHWAY: BIOSYNTHESIS OF D-ALANYL-LIPOTEICHOIC ACID.
I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
I- SIMILARITY: TO 3-OXOCYL-[ACYL-CARRIER PROTEIN] REDUCTASES.
I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLASER P., KUNST F., ARNAUD M., COUDART M.P., GONZALES W.,
HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., MOSZER I.,
PRESECAN E., SANTANA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
RAPOPORT G., DANCHIN A.;
"Bacillus subtilis genome project: cloning and sequencing of the
"Bacillus subtilis genome project: cloning and sequencing of the
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95318144.
PEREGO M., GLASER P., MINUTELLO A., STRAUCH M.A., LEOPOLD K.,
PISCHER W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-168;
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252 AA;
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TGGSAGIGLE LAKRLLELGN EVIICGRSEA RLAEAKQQLP
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                                                                                      NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
; CC2A1A1D CRC32;
                                                                                                                                                                                                                                                                                                                                                         removed. Usage by and for commerciation (See http://www.isb-sib.ch/announce/
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DISULFIDE BOND FORMATION PROTEIN B (DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation and the EMBL outstation on the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Busage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P28562;
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Bacteria; Proteobacteria;
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TRANSMEM
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DUS1_HUMAN
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mitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOME
PERIFLASMIC PROTEINS SUCH AS PHOA OR OMPA. ACTS BY OXIDIZING
THE DSBA PROTEIN (BY SIMILARITY).
GIRCHILLIAN TO TOTAL TOTAL THE DSBA PROTEIN (BY SIMILARITY).
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CYTOPLASMIC (
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CYTOPLASMIC (POTENTIAL)
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PHOSPHATASE
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IIAA_SEQUENCE 1.0
ID DUS1_MOUSE
AC P28563;
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PIR; S29090; S29090
HSSP: P51452; 1VHR.
MIM; 600714;
PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE: PS50056; TYR_PHOSPHATASE_DUAL; 1.
                                          Ol-DEC-1992 (Rel. 24, Created)
Ol-DEC-1992 (Rel. 24, Last sequence update)
Ol-NOV-1997 (Rel. 35, Last annotation update)
DUAL SPECIFICITY PROTEIN PHOSPHATASE 1 (EC 3.1.3.48)
(MAP KINASE PHOSPHATASE-1) (MEK-1) (PROTEIN-TYROSINE 3CH134) (PROTEIN-TYROSINE PHOSPHATASE ERP).
DUSPI OR PIPNIO OR MKP1 OR 3CH134 OR PTPNI6.
Eutheria; Rodentia; [1]
                            Eukaryota; Metazoa;
                                      Mus musculus (Mouse)
                                                                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Cell cycle.
DOMAIN 175 367
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REYES S.M., EMSILE E.A.;

ROYAL STRESS and heat shock induce a human gene encoding a protein-tyrosine phosphatase.",

Nature 359:644-647(1992),

I FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES INTUSED BEACH THR-183 AND TYR-185.

I CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + DESPRIATE STRESS AND HEAT SHOCK.

INDUCTION: BY OXIDATIVE STRESS AND HEAT SHOCK.

TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFRMILY.

TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFRMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00581; Rhodanese; 1. PFAM; PF00782; DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93024952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NSALSYLQSP
                                                                                                                                                                                                                                                       FMGQLLQFES
                                                                                                                                                                                                                                                                                GGRVFVHCQA GISRSATICL
                                                                                                                                                                                                                                                                                                                                                                         TLALAAGALC
                                                                                                                                                                                                                                                                                                                                                                                               IVRRRAKGAM GLEHIVPNAE LRGRLLAGAY HAVVLLDERS AALDGAKRDG
                                                                                                                                                                                                                                                                                                                                               TSVPDSAESG
                                                                                                                                                                                                                                                                                                                                                                                                                                   MVMEVGTLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
367 AA;
                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                         ITTSPSC
                                                                                                                                                                                                                                                QVLAPHCSAE AGSPAMAVLD
                                                                                                                                                                                                                                                                                                                                                                                                                            GGLRALLGER AAQCLLLDCR SFFAFNAGHI AGSVNVRFST
                                                                                                                                                                                                                                                                                                              PNHFEGHYQY
                                                                                                                                                                                                                                                                                                                                            CSSCSTPLYD
                                                                                                                                                                                                                                                                                                                                                                        REARAAQVFF
       Chordata; Craniata; Ve
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 CATALYTIC.
258 BY SIMILARITY.
39297 MW; DA323420 CRC32;
                                                                                                                                                                                                                                                                                                                                                                 LKGGYEAFSA SCPELCSKQS TPMGLSLPLS
                                                                                                                                                                                                                                                                              AYLMRTNRYK LDEAFEFVKQ
                                                                                                                                                                                                                                                                                                            KSIPVEDNHK
                                                                                                                                                                                                                                                                                                                                            QGGPVEILPF
                                                                                                                                                                            PRT;
                                                                                                                                                                          367
                                                                                                                                                                                                                                              RGTSTTTVFN FPVSIPVHST
                                                                                                                                                                                                                                                                                                          ADISSWFNEA
                                                                                                                                                                                                                                                                                                                                        LYLGSAYHAS
       Vertebrata;
ae; Murinae;
                                                                                                                                                                        À
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                                                                                                                                                                                                                                                                                                          IDFIDSIKNA
                                                                                                                                                                                                                                                                                                                                     RKDMLDALGI
                                                                           (EC 3.1.3.16)
PHOSPHATASE
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DUS1_MOUSE
                                                                                                                                                                                                                                                                                                                                              RY CHARACTERIZATION.

RX SUM H, CHARLES C.H., LAU L.F., TONKS N.K.;

RX SUM H, CHARLES C.H., LAU L.F., TONKS N.K.;

RY SUM H, CHARLES C.H., LAU L.F., TONKS N.K.;

RY SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP CEL 175:487-493(1993).

CC 1- FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP CEL 175:487-493(1993).

CC 1- INDUCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP CEL 175:487-493(1993).

CC 1- INDUCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES MAP CEL 1700 THE NON-RECEPTOR CLASS OF THE PROTEIN TYROSINE PHOSPHATE.

CC 1- INDUCTION: BY GROWNH PACTORS.

CO 2- INDUCTION: GROWNH PACTORS.

CO 2- INDUCTION: GROWNH PACTORS.

CO 2- INDUCTION: GROWNH PACTORS.

CO 2
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MEDLINE; 93360956.
MEDLINE; 93360956.
MOGUCHI T., METZ R., CHEN L., MATTEI M.-G., CARRASGO D., BRAVO R.;
"Structure, mapping, and expression of erp, a growth factor-inducible gene encoding a nontransmembrane protein tyrosine phosphatase, and effect of ERP on cell growth.";
Mol. Cell. Biol. 13:5195-5205(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C;
MEDLINE; 92158357.
MEDLINE; 92158357.
CHARLES C.H.; ABLER A.S., LAU L.F.;
"CDNA sequence of a growth factor-inducible immediate characterization of its encoded protein.";
Oncogene 7:187-190(1992).
                                                                                                                                                                                                                                                     MVMEVGILDA GGLRALLREG
                                                                                                                                                                                                                                                                                                Length: 367
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258
258
367 ;
                                                                                                                                                                                                                                                                                                                                       AA;
    QVLAPHCSAE
                                             GISRSATICL
                                                                                                                                                                                                            GLEHIVPNAE
                                                                                                                             CSSCSTPLYD
                                                                                                                                                                   REARSTOVFF
                                                                                                                                                                                                                                                                                    February 14, 2000 08:02 Type: P
                                                                                                                                                                                                                                                                                                                               258 C->S: LOSS OF ACTIVITY 39369 MW; 17B905B5 CRC32;
    AGSPAMAVLD
                                    AYLMRTNRVK LDEAFEFVKQ RRSIISPNFS
                                                                                 KSIPVEDNHK
                                                                                                                          QGGPVEILSF
                                                                                                                                                                   LQGGYEAFSA
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                                                                                                                        LYLGSAYHAS
RGTSTTTVFN FPVSIPVHPT
                                                                               ADISSWFNEA
                                                                                                                                                                 SCPELCSKQS
                                                                                                                   RKDMLDALGI
                                                                                                                                                                                                     ASLDGAKRDG
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iiAA_SEQUENCE 1.0
ID DYR1_BRARE
AC P35621;
DT 01-UUN-1994 ()
DT 15-JUL-1999 ()
DT 15-JUL-1999 ()
DE DVR-1 PROTEIN
GN VG1 OR DVR-1.
OS Brachydanio rr
OC Eukaryota; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUS1_RAT
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Created)
01-N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its concent is in modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
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                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DVR-1 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
      Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIM-SPRAGUE-DAWLEY; TISSUE-LUNG;
AIM-SPRAGUE-DAWLEY; TISSUE-LUNG;
AIM-SPRAGUE-DAWLEY; TO tHE ENEL/GenBank/DDBJ databases.

mitted (JAN-1995) to the ENEL/GenBank/DDBJ databases.

mitted (JAN-1995) to the ENEL/GenBank/DDBJ databases.

FUNCTION: DUAL SPECIFICITY PHOSPHATASE THAT DEPHOSPHORYLATES NEUTRINGSINE PROSPHATE H(2)0 =

CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE.

PROTEIN TYROSINE ORTHOPHOSPHATE.

SIMILARITY: BELONGS TO THE MON-RECEPTOR CLASS OF THE PROTEIN-

TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.

TYROSINE PHOSPHATASE FAMILY. DUAL SPECIFICITY SUBFAMILY.
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                                                                    OR DVR-1
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ota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00383; TYR_PHOSPHATASE_1; 1.
PS50056; TYR_PHOSPHATASE_2; 1.
PS50054; TYR_PHOSPHATASE_DUAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
367 1
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; DSPC; 1.
11 cycle.
75 367
78 258
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39541 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
BY SIMILARITY.
; 9DE266E3 CRC32;
                    (Zebra danio)
Craniata; Vertebrata;
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
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Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 3.1.3.16)
PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Check:
                       Actinopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6443
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                                  II AA_SEQUENCE 1.0
ID E128_DROME
AC P08761;
DT 01-NOV-1988 (I
DT 01-NOV-1988 (I
DT 01-OCT-1996 (I
                                        P08761;

P08761;

01-NOV-1988 (Rel. 09, Created)

01-NOV-1988 (Rel. 09, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                     351
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ECGCR

STANDARD;

255

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DVR1_BRARE
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"The DVR-1 (Vg1) transcript o
distributed throughout the em
Dev. Biol. 159:418-426(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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HSSP; P18075; IBMP 25-389; VG1.
ZFIN; ZDB-GENE-980526-389; VG1.
PROSITE; PS00250; TGT_BETA; 1.
PFAM; PE00019; TGT-beta; 1.
Growth factor; Mitogen; Glycopomental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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301
                                          251
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                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER MESODERM OR ENDODERM SITHER AS A COFACTOR IN AN INSTRUCTIVE SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISTRIBUTED AMONG ALL BLASTOMERES.

DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CLEAVAGE AMONG ALL CUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL CELLS OF THE BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEVAGE, BLASTULA AND GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE GASTRULA STAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GASTRULA
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                                                                                                                                   LKGVTHESSR
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AILQTLVHSF
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                                                                                                                                                                                                                                                                  LTLSLCSPAE DDGLVQEKLF LSSMGLWSRP KPSHHAAVPS
                                                                                                                                      KLLQSQTLSP
                                                                                                                                                                                VLEEVEQLSL
                                                                                                                                                                                                                           KQTVNDPCVV
  DPKGTPQPCC
                                               IDFKDVGWQD
                                                                                       DHAYVQIPDI
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     VPIKLSPISM
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BY SIMILARITY
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BY SIMILARITY.
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POTENTIAL.
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       LYYDNNDNVV LRHYEDMVVD
                                                                                               PLQCRSRRKR
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MBL outstation -
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ECDYSONE-INDUCED PROTEIN 28/29 EIP28/29.

(Fruit fly)

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EI28_DROME Length: 255 February 14, 2000 08:02 Type: P Check:
SEQUENCE FROM N.A., AND SEQUENCE OF 21-30.

TISSUE-MAMMARY GLAND;

PIOTTE C.P., GRIGOR M.R.;

PIOTTE C.P., GRIGOR M.R.;

"A novel marsupial protein expressed by the mammary gland only during the early lactation and related to the Kunitz proteinase inhibitors.";

the early lactation and related to the Kunitz proteinase inhibitors.";

-I- SUBCELLULAR LOCATION: SECRETED.

-I- SUBCELLULAR LOCATION: SECRETED.

-I- DEVELOPMENTAL STAGE: EXPRESSED ONLY DURING EARLY LACTATION PHASE.

-I- TISSUE SPECIFICITY: EXPRESSED BY THE MAMMARY GLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X58286; CAA41223.1; -.
EMBL; X04024; CAA27658.1; -.
EMBL; X04024; CAA27658.1; -.
EMBL; X04521; CAA28205.1; -.
PIR; A24254; A24254
FLYBASE; FB9n0000565; Eip71CD.
PFAM; PF01625; PMSR; 1.
Alternative splicing.
VARSPLICT 252 252
SEQUENCE 255 AA; 28332 MW; 6
                                                                                                                                     Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                                                                            ELAC_TR
Q29143;
                                                                                                                                                                                              15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
EARLY LACTATION PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                       SEQUENCE 1.0
ELAC_TRIVU
                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"I NOIL BAOL 189:617-631(1986).
"I INDUCTION: BY ECDYSONE."
"STMILARITY: TO BACTERIAL AND EUKARYOTIC PEPTIDE METHIONINE SULFOXIDE REDUCTASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                         KENFYPAEAY HQKYRLQGHK DLASSLNLSP KLLQTSYVAT
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V -> L (IN MRNA).
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IIAA_SEQUENCE 1.0
ID ERP2_YEAST
AC P39704;
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                                                                                                                                                                                                      CHARACTERIZATION.

CHARACTERIZAT
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MEDILINE; 95028152.

CLARK M.W., KENG T., STORMS R.K., ZHONG W., FORTIN N., ZENG B.,

DELANEY S., OUELLETTE B.F.F., BARTON A.B., KABACK D.B., BUSSEY H.;

"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis c

the 42 kbp SPO7-CENI-CDC15 region.";

Yeast 10:555-541(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ERP2 PROTEIN PRECURSOR.
ERP2 OR YALOO7C OR FUN54.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease inhibitor; S. SIGNAL 1 20 CHAIN 21 102 DISULFID 43 93 DISULFID 52 76 DISULFID 68 89 ACT_SITE 53 54 CARBOHYD 34 CARBOHYD 34 CARBOHYD 34 CARBOHYD 34 SEQUENCE 102 AA; 11407 MW;
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DISULFID
DISULFID
DISULFID
ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REACTIVE BOND (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
MW. D7983676 CRC32;
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                                                                                  There are no restrictions on ng as its content is in no
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                                                                                                                                                         a collaboration -
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SOUR STANDS
                                                                                                 ERP2_YEAST
                                                                          ES1_BRARE
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ES1_BRARE
Q90257;
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PIR; $40896; $40896;

SGD; L0004679; ERP2.

PFAM; PF01105; EMP24_GP25L;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterydi; Teleostei; Buteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                                                  CHANG H., GILBERT W.;

"A novel zebrafish gene expressed specifically in the photoreceptor
"A novel zebrafish gene expressed specifically in the photoreceptor
cells of the retina.";

Biochem. Biophys. Res. Commun. 237:84-89(1997).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (POTENTIAL).
-!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN PHOTORECEPTOR CELLS
OF THE RETINA.

OF THE RETINA.

OF THE RETINA.

OF THE RETINA.
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                                                                                                                                    EMBL; U10403; AAC60261.1; TETIN; ZDB-GENE-980526-188; ES1.
Mitochondrion; Transit peptide.
TRANSIT 1 7 MI;
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S40896
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                                                                             270
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                                                                                                      AA;
MMQMNDLSKL DANSFDAVIF PGGHGIVKNM STFSKDGKDO
                                                QAAAMLVRQP
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                                                                           February 14,
                                                                                                        30685 MW;
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                                                    ACLMHHGGDW
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50CD1406 CRC32;
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POTENTIAL.
                         QIFAPNQQQM
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                                                                                                                    MITOCHONDRION (POTENTIAL).
ES1 PROTEIN.
                                                                                                         S1 PROTEIN
4B69565D
                                                                              2000 08:02
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                                                                                                                                                                                                                  (See http://www.isb-sib
                                                       GNWGNTNIAV VFSGCGWWDG
                          HVMDHMKMQP
                                                                                                           CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signal;
                                                                              Type:
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                              SSSDNRNIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cypriniformes;
                                                                                  Check:
                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                          a collaboration -
                                                                                                                                                                                                                                   commerciai
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ETFA_MYCLE Length:

318

February 14, 2000 08:02 Type: P Check:

3764

Electron transport; NP_BIND 257 SEQUENCE 318 AA;

; Flavoprotein; FAD. 285 FAD (ADP PART) (POTENTIAL) 31837 MW; 9CF35B35 CRC32;

101

SGLLVDVVDV AESDAADKYL

REGAVGVHSV ITPVVDVLAA

FGGVFIVEAQ ANGDTPVITV

LAESSAPAAV

LLAATADGKE

EPAAVVVGTP GTSAPLVDGL

EGAGEQVSVE

ITARAPAVVD

NRPDLTEAT

51 ш

KTAGAAKIYV

MAEALVLVEH TEGALKKVSA ELITAARVLG

201 151

101

ROSSEDITA

15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last seq 15-DEC-1998 (Rel. 37, Last ann

sequence up annotation

IOPOLYMER TRANSPORT EXBD

Bacteria; [1]

gonorrhoeae.
proteobacteria;

beta

subdivision; Neisseriaceae;

! AA

SEQUENCE 1.0

EXBD_NEIGO O06434;

STANDARD;

PRT;

144

A

301

DLFKVAPQLT KTVSPQLYIA **VVSGGRGVGS**

DGIKARKG LGISGAIQHR ADNESVVEAL

> AGMQTSKTIV ADSLGAAVGA VPAPAENATK

AVNKDEEAPI FEIADFGVVG SRAAVDSGYY PGQFQIGQTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last sequence update)
ELECTRON TRANSFER FLAVOPOTEIN ALPHA-SUBUNIT (
TRANSFER FLAVOPROTEIN LARGE SUBUNIT) (ETFLS).
ETFA OR FIXE OR MLCBG37.04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                             EMBL; Z99263; CAB16419.1; -. PROSITE; PS00696; ETF_ALPHA; 1. PFAM; PF00766; ETF_alpha; 1.
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EXBD_NEIGO Length: 144 February 14, 2000 08:02
                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-SEROGROUP C;

MEDLINE; 97158676.

MEDLINE; 97158676.

STOJILJKOVIC I., SRINIVASAN N.;

"Neisseria meningitidis tonb, exbb, and exbb genes: Ton-dependent utilization of protein-bound iron in Neisseriae.";

J. Bacteriol. 179:805-812(1997).

J. Bacteriol. 179:805-812(1997).

J. Bacteriol. 179-KOSTENES ENERGY-DEPENDENT TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

COMPLEX WITH TONB (BY SIMILARITY).

J. SUBCELLULIAR LOCATION: TYPE II MEMBRANE PROTEIN. INNER MEMBRANE
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                                                                                                                         (PROBABLE).
-!- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U79563; AAC45288.1; ..

Transport; Protein transport; Transmembrane; Inner membrane.
DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).

TRANSMEM 19 39 POTENTIAL.

DOMAIN 40 144 PERIPLASMIC (POTENTIAL).

TRANSMEM 40 144 PERIPLASMIC (POTENTIAL).

TRANSMEM 40 144 PERIPLASMIC (POTENTIAL).
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P5376;
P5376;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
BIOPOLYMER TRANSPORT EXBD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                 EXBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BISWAS G.D.,
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SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.
 U77738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNENVIVAIA ADKAVEYDYV NKALEAARQA GITKIGFVTE
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AAC44836.1;
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I!AA_SEQUENCE 1.0

ID FABG_ECOLI

AC P25716; PF8621

DT 01-MAY-1992 (R

DT 01-MOY-1997 (R

DT 01-NOV-1997 (R

DE 3-OXOACYL-[ACY

DE SCHERICH; P201

OC ESCHERICH; P201

OC ESCHERICH; P201

OC BACTERIA K.2;

RN [1]

RN [2]

RN [2]

RN [2]

RN SEQUENCE FROM

RC STRAIN-K12;

RX MEDLINE; 974

RA RATILET M., CC

RA GREGOR J., C

RA MADLINE; 974

RA MADLINE; 977

RA SAMPEI G., (C

RA SAMPEI G., (C

RA SAMPEI G., (C

RA YANO M., H(

RA Y
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SAMDI K., KANAI K., KANIMOTO K., KANIMOTO K., KANIMOTO K., KANIMOTO K., KANIMOTO K., KANIMOTO K., SAITO N., SAITO N., SAITO N., SAITO N., SAITO N., SAITO N., HORIUCHI T.;

YANO M., HORIUCHI T.;

YANO M., HORIUCHI T.;

YANO M., HORIUCHI T.;

SAMDI G., STRAIN SAMUENCE OF The Escherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                              SAMPET G. SEKIY. MARAMURA I., NASHIOYU H., NISHIO Y., SAITO YANO M., HORIUCHI T., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).

-I- CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] H. NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.

-I- PATHMAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS PATHMAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRALN=K12 / MG1655;
MEDLINE; 97428617.
MEDLINE; 97428617.
MEDLINE; 97428617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92210530.

RAWLINGS M., CRONAN J.E. JR.;

"The gene encoding Escherichia coli acyl carrier a cluster of fatty acid biosynthetic genes.";

J. Biol. Chem. 267:5751-5754(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P25716; p78221;
01-MAY 1992 (Rel. 22, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
3-OXCACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-CARRIER PROTEIN REDUCTASE).
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STRAIN-K12;
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNENVIVAIA ADKAVEYDYV NKALEAARQA GITKIGFVTE
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15514 MW;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
6347F02B CRC32;
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There are no restrictions on ng as its content is in no

collaboration -

EMBL; M84991; AAA23739.1;

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THE TRANSPORT OF THE PROPERTY 
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EMBL; D90745; BA2
PIR; B42147; B42
HSSP; P19992; 2H
ECOGENE; EG11318
PROSITE; PS00061
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (ECACYL CARRIER PROTEIN REDUCTASE).
FABG OR HI0155.
                       EMBL; U32701;
HSSP; P19992;
TIGR; HI0155;
                                                                                                                                                                                                                                                                                                                                                                                        FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BUIT C.J., TOMB J.-F., DOUGHERRY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WELDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., FINE L.D., KELLEY J.M., SMALL K.V., FRASER C.M., SMITH H.O.,
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-RD / KW20; MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and assembly of Haemophilus \inf \operatorname{Lenzae} \ \operatorname{Rd}.
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  PS00061; ADH_SHORT;
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'45; BAA35901.1;
7; B42147.
                                                                        AAC21824.1;
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25560 MW;
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A -> G (IN REF. 1).
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                                                                                                                                                      FABG_PSEAE
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FABG_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PAO1;
KUTCHNA A.J., HOANG T.T., SCHWEIZER H.P.;
KUTCHNA A.J., HOANG T.T., SCHWEIZER H.P.;
Submitted (FEB-1997) to the EMEL/GenBank/DDBJ databases.

NADP(+) = 3-0XOACYL-[ACYL-CARRIER PROTEIN] + NADPH.

NADP(+) = 3-0XOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
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PFAM; PF00678; adh_short_C2; 1.

Fatty acid biosynthesis; Oxidoreductase; NADP.

NP_BIND 8 2 NADP (BY SIMILARITY)

ACT_SITE 149 149 BY SIMILARITY.

SEQUENCE 242 AA; 25507 MW; CBFCAFD9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no result use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsensenal to license@isbsib.ch).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE (ECACYL CARRIER PROTEIN REDUCTASE).
                                                                                                                                                                                                        EMBL: U91631; AAB94395.1; -.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_Short_C2; 1.
FFAM; PF00678; adh_Short_C2; 1.
FFATY acid biosynthesis; Oxidoreductase; NP_BIND 10 34 NADP (BY SIN NP_BIND 154 BY SINILARII 155 BY SI
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STRAIN-PAO1;
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Bacteria; Proteobacteria;
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                                                                                                       MSLQGKVALV TGASRGIGQA
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SKAVLRGMTK
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ARWGRIINIG
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MBL outstation -
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HSSP; P19992; 2HSD.
PROSITE; PSO0061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
PFAM; PF000678; adh_short; 2:
PATTY acid biosynthesis; Oxidored NP_BIND 10 34 NADP ACT_SITE 151 BY SEQUENCE 244 AA; 25519 MW; AE
                                                                                                                                                                                                             P28861: p11007:
01-UUI-1989 (Rel. 11, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
FERREDOXIN--NADP REDUCTASE (EC 1.18.1.2) (FNR) (FL
                            SEQUENCE FROM N.A.,
STRAIN=K12 / C600;
STRAIN=K12 / C600;
MEDLINE; 93194782.
BIANCHI V., REICHARI
                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                               (FLXR) (FLDR) (METHYL FPR OR MVRA. Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FENR_ECOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHEN Z., BYERS D.M.;
"Isolation of Vibrio harvey1 acy1 carrier protein and the fabG, acy and fabF genes involved in fatty acid biosynthesis.";
J. Bacteriol. 178:571-573(1996).
J. Bacteriol. 178:571-573(1996).
J. CATALYTIC ACTIVITY: (3R) 3-HYDROXYACYL-[ACYL-CARRIER PROTEIN]
NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
J. SOMACYL- REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-B392;
MEDLINE; 96134997.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
3-0XOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE (ECACYL CARRIER PROTEIN REDUCTASE).
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P55336;
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  Ή.
REICHARD P., ELIASSON R.,
, HAGGARD-LJUNGQUIST E.;
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                                                                                               SEQUENCE
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NADP (BY SIMILARITY).
BY SIMILARITY.
9 MW; AE981EDC CRC32;
                                                                                                                                                                        gamma subdivision;
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MEDLINE: 97233095.

MAINTENAN M. BLANCHI V. EXUND H;
MINGELMAN M., BLANCHI V. TOULD H;
MINGELMAN M., TOULD H;
MINGELMAN M., TOULD H;
MINGELMAN M. TOULD METHININE SYNTHASE, PYROUAN;
MINGELMAN METHININE SYNTHASE, PYROUAN;
MINGELMAN METHININE SYNTHASE, PYROUAN;
MINGELMAN METHININE SYNTHASE, PYROUAN;
MINGELMAN METHININE STANDHAMIN INDEPENDICH METHYL VIOLOGEN IN METHINING MET
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and characterization of Escherichia coli K-12.";
Of Bacteriol. 170:2136-2142(1988).
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MEDLINE 93015762
TRUNIGER V., BOOS W., SWEET G.;
"Molecular analysis of the glpFKX
Shigella flexner: ",
J. Bacteriol. 174:6981-6991(1992).
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"Flavodoxin and NADPH-flavodoxin reductase from Escherichia coli
"prodoxin and NADPH-flavodoxin reductase from Escherichia coli
support bovine cytochrome P450c17 hydroxylase activities.";
J. Biol. Chem. 269:27401-27408(1994).
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MEDLINE; 95050480.
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PLUNKETT G. III, BURLAND V.D., DANIELS D.L., B
"Analysis of the Escherichia coli genome. III.
region from 87.2 to 89.2 minutes.";
Nucleic Acids Res. 21:3391-3398(1993).
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STRAIN=K12 / N
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EMBL; L04757; AAA23805.1; -.
EMBL; L19201; AAB03056.1; -.
EMBL; AE000467; AAC75066.1; -.
EMBL; Z11767; -; NOT_ANNOTATED_CDS.
EMBL; M19644; AAA24189.1; ALT_SEQ.
PIR; A42625; A26225.
PIR; B45248; B45248.
PIR; B45248; B45248.
PIR; A47077; AA7077.
PIR; S40867; S40867.

AYSYVNSPDN

PDLEFYLVIV

PDGKLSPRLA ALKPGDEVQV VSETAGFFVL

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FENR_ECOLI Length: 247 February 14, 2000 08:02
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ECCGENE; EG11518; FPR.
FPAM; PP00175; oxidored_fad; 1.
PFAM; PF00175; oxidored_fad; 1.
Oxidoreductase; Flavoprotein; NADP; FAD; 3D-Structure.
INIT_MET 0 0 FAD.
NP_BIND 49 75 FAD.
NP_BIND 109 125 NADP (RIBOSE PART) (BY S
NP_BIND 109 125 NADP (RIBOSE PART) (BY S
NP_BIND 109 125 NADP (RIBOSE PART) (BY S
                                                                                                                                                                                                                                                                                                                           "Molecular analysis of the glpFKX regions of Escherichia coli and Shigella flexneri.";

J. Bacteriol, 174:6981-6991(1992),

-i. FUNCTION: TOGETHER WITH FLAVODOXIN IS INVOLVED IN THE REDUCTIVE ACTIVATION OF COBALAMIN-INDEPENDENT METHIONINE SYNTHASE, PYRUVATE FORMATE LYASE AND ANAEROBIC RIBONUCLEOTIDE REDUCTASE. ALSO PROTECTS AGAINST SUPEROXIDE RADICALS DUE TO METHYL VIOLOGEN IN THE PRESENCE OF OXYGEN (BY SIMILARITY).

-i. CATALYTIC ACTIVITY: REDUCED FERREDOXIN + NADP(+) - OXIDIZED FERREDOXIN + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Kel. 37, Last annotation update) FERREDOXIN-NADP REDUCTASE (EC 1.18.1.2) (FNR) (FLXR) (METHYL VIOLOGEN RESISTANCE PROTEIN A) (FLX.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P28901,
01-DEC-1992 (Rel. 24, Created)
01-JUL-1993 (Rel. 26, Last seq)
15-DEC-1998 (Rel. 37, Last ann
15-DEC-1998 (Rel. 37, Last ann
FERREDOXIN--NADP REDOCTASE (ST
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FENR_SHIFL
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Oxidoreductase; Flavoprotein; NADP; FAD. NP_BIND 50 76 FAD (BY SIM NP_BIND 110 126 NADP (RIBOS NON_TER 135 135 SEQUENCE 135 AA; 14878 MW; F6A7AD5D
                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                                                                                               EMBL; Z11766; CAA77813.1; ALT_SEQ.
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; P28861; 1FDR.
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   F6A7AD5D CRC32;
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(RIBOSE PART)
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FENR_SHIFL Length: 135

February 14,

2000

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Type:

gamma

subdivision; Enterobacteriaceae;

MADWVTGKVT KVQNWTDALF SLTVHAPVLP FTAGQFTKLG LEIDGERVQF

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FIMH_SALTY
P37925;
01-0CT-1994 (
01-0CT-1994 (
15-DEC-1998)
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p18891;

p1-DEC-1992 (Rel. 24, Created)

01-DEC-1994 (Rel. 28, Last sequence update)

01-NOV-1995 (Rel. 32, Last annotation update)

p1-NOV-1995 (Rel. 24, Created)

p1-NOV-1995 (Rel. 24
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Salmonella typhimurium.
Bacteria; Proteobacteria;
Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF01421; Reprolysin; ydrolase; Metalloprotease;
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                                                                   (Rel. 30, C)
(Rel. 30, L)
(Rel. 37, L)
(N PRECURSOR.
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                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                           LVIVADHRMN TKYNGDSDKI RQWVHQIVNT
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                                                                                  30, Created)
30, Last sequence update)
37, Last annotation update)
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T -> L.
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ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
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DC49D0E9 CRC32;
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SOME % OF THE CHAINS).
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SEQUENCE FROM N.A.
SWENSON D.L., CLEGG S.;
SWENSON D.L., CLEGG S.;
SWENSON D.L., CLEGG S.;
SWENSON D.L., CLEGG S.;
SUBMITTED (JUN-1993) to the EMBL/GenBank/DDBJ databases.

-i. FUNCTION: INVOLVED IN REGULATION OF LENGTH AND MEDIATION OF ADHESION OF TYPE 1 FIMBRIAE (BUT NOT NECESSARY FOR THE PRODUCTION OF FIMBRIAE). SEEMS TO BE MANNOSE BINDING ADHESIN.

-i. SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

-i. SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

-i. SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

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-i. SIMILARITY: BELONGS TO THE FIMH / LEFD FAMILY.

-i. SIMI
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               polypeptide.";
J. Bacteriol: 173:3573-3579(1991).
-!- FUNCTION: NEEDED FOR FLAGELLAR REGROWTH AND ASSEMBLY.
-!- SIMILARITY: TO FLIH IN OTHER BACTERIA AND ALSO TO FILI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
Bacillus firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91258343.
ALBERTINI A.M., CARAMORI T., CRABB W.D., SCOFFONE F., GALIZZI A.;
"The flaA locus of Bacillus subtills is part of a large operon coding for flagellar structures, motility functions, and an ATPase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE FLAGELLAR ASSEMBLY PROTEIN FLIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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335 AA;
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335 F
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FIMH PROTEIN.
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EMBL; X56049; CAA39522.1; -. EMBL; Z99112; CAB13496.1; -.

!!AA_SEQUENCE 1.0

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FOS_AVINK Length: 322 February 14, 2000 08:02 Type: P
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#IR: B34071; TYFVF4.

HSSP; P01100; IFCS.

#RANUSPAC: T01453;

PROSITE: P050036; BZIP_BASIC; 1.

#FAM; PF00170; bZIP; 1

#FAM; PF00170; DNA-binding.

#FMSIC MOTIF.

BASIC MOTIF.

BOMAIN

119

147

LEUCINE-ZIPPER.

#FMSIC MOTIF.

BASIC MOTIF.

#FMSIC MOTIF.

BASIC MOTIF.

#FMSIC MOTIF.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 88062920.

NISHIZAWA M., GOTO N., KAWAI S.;

"An avian transforming retrovirus isolated from a nephroblastoma that carries the fos gene as the oncogene.";

J VIOL 61:3733-3740(1987).

1- SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P23050;
01:NOV-1991 (Rel. 20, Created)
01:NOV-1991 (Rel. 20, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
P55-Y-FOS TRANSFORMING PROTEIN.
                                                                                                                                                                                                                                                                            51
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Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.
[1]
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PIR; C42365; C42365.
SUBTILIST; BG10242; FLIH.
Flagella.
SEQUENCE 208 AA; 23788
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RKGSSSNEPS
                                                       WEPLGAGSGG
                                                                                                                                                                  LAAHRPACKM
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                                                                                                                                                                                                                                                                         GVPAPAPPAA YSRPAVLKAP
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                                                       ELEPLCTPVV
                                                                                                       GLELKAEPFD ELLFSAGPRE
                                                                                                                                                              PEELRFSEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44B8A68A CRC32;
                                                                                                 ASRSVPDMDL
                                                                                                                                                                                                                                                                      GKVEQLSPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322
                                                                                                                                                           PSPAAAEEAF
                                                                                                 PGASSFYASE
                                                                                                                                                                                                               LKEKEKLEFI
                                                                                                                                                                                                                                                                                                                          APSQNRGHPY
                                                                                                                                                        ALPLMTEAPE
                                                                                                                                                                                                                                                                   EEKRRIRREF
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FOS_CHICK
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P11939;
01-OCT-1989
01-OCT-1989
01-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOELDERS H., JENUWEIN T., ADAMKIEWICZ J., MUELLER R.;
"Isolation and structural analysis of a biologically active chicken c-fos cDNA: identification of evolutionarily conserved domains in fos protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence up
01-OCT-1986 (Rel. 34, Last annotation
p55-C-FOS PROTO-ONCOGENE PROTEIN.
                                                                                                                                                                                                                  Proto-oncogene; Nuclear protein; Phosphorylation;
DNA_BIND 138 159 BASIC MOTIFE
DOMAIN 164 152 LEUCINE-ZIPPER.
CONFLICT 90 90 N -> D (IN REF. 2).
SEQUENCE 367 AA; 39004 MW; A3FCDACB CRC32;
301
                            251
                                                       201
                                                                                151
                                                                                                           101
                                                                                                                                                                                                                                                                                    PROSITE; PS00036; BZIP_BASIC; 1.
PFAM; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                    TRANSFAC;
PROSITE; F
                                                                                                                                                                                                                                                                                                                                       EMBL; M37000; AAA48670.1; -.
EMBL; M18043; AAA76823.1; -.
EMBL; A28368; TVCHFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 1:377-385(1987).
                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A. EDLINE; 88262231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR.
INDUCTION: C-FOS EXPRESSION INCREASES RAPIDLY UPON GROWTH FACTOR STIMULATION OR WOUNDING OF CULTURED CELLS.
SIMILARITY: TO OTHER BZIP PROTEINS.
                                                                                                          APPAAYSRPA VLKAPGGRGQ
                                                                                                                                                               MMYQGFAGEY EAPSSRCSSA
                                                       PACKMPEELR
                                                                                                                                      TDLAVSSANF
                                                                                                                                                                                         Length: 367
 AGSGGELEPL CTPVVTCTPC
                            EPSGSGLELK
                                                                                                                                                                                                                                                                                                                   T00125;
                                                                                                                                                                                                                                                                                                                               1FOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                      VPTVTAISTS
                                                       FSEELAAATA
                            AEPFDELLFS
                                                                                TOTLQAETDQ
                                                                                                                                                                                          February 14, 2000 08:02 Type: P
                                                                                                                                    PDLQWLVQPT LISSVAPSQN
 PSTYTSTFVF TYPEADAFPS CAAAHRKGSS
                            AGPREASRSV
                                                       LDLGAPSPAA
                                                                                LEEEKSALQA
                                                                                                           SIGRRGKVEQ
                                                                                                                                                               SPAGDSLTYY
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on update)
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                                                                                                                                                                 PSPADSFSSM
                            PDMDLPGASS FYASDWEPLG
                                                                                  EIANLLKEKE
                                                                                                           LSPEEEEKRR
                                                       AEEAFALPLM
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                                                                                                                                                               GSPVNSQDFC
                                                                                  KLEFILAAHF
                                                                                                             IRRERNKMAA
                                                                                                                                      RGHPYGVPAP
                                                       TEAPPAVPPK
                                                                                                                                                                                                                                                                         DNA-binding
                                                                                                                                                                                          Check: 7007
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!!AA_SEQUENCE 1.0

351

SNEPSSDSLS

SPILLAL

!!AA_SEQUENCE 1.0

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STIRE REPRESENTATION OF THE STREET OF THE ST
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MEDLINE; 83221560
VAN STRAATEN F., MULLER R., CURRAN T., VAN BEVEREN
"Complete nucleotide sequence of a human c-onc gene
acid sequence of the human c-fos protein.";
proc. Natl. Acad. Sci. U.S.A. 80:3183-3187(1983).
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P01100;
P01100;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
P55-C-FOS PROTO-ONCOGENE PROTEIN (GOS7 PROTEIN)
351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V01512; CAA24756.1; -.
EMBL; K00650; AAA52471.1; -.
PIR; A01342; TVHUF1
PDB; 1FOS; 10-JUL-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- INDUCTION: C-FOS EXPRESSION INCREASES RAPIDLY UPON GROWTH FACTOR STIMULATION OR WOUNDING OF CULTURED CELLS.
-!- SIMILARIY: TO OTHER BLIP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLOVER J.N., HARRISON S.C.;
"Crystal structure of the heterodimeric bZIP
"-FOS-C-Jun bound to DNA.";
Nature 373:257-261(1995).
"I- FUNCTION: C-FOS IS A NUCLEAR PHOSPHOPROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Jomo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Sutharia: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RAY CRYSTALLOGRAPHY (3.05 ANGSTROMS) OF 139-198 EDLINE; 95115802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coto-oncogene; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: C-FOS IS A NUCLEAR PHOSPHOPROTEIN WHICH NON-COVALENTLY LINKED COMPLEX WITH THE C-JUN/AP-1
FPSCAAAHRK
                                                                                                                                                                                                                                                                                                                                                                             MMFSGFNADY EASSSRCSSA
                                                     ADWEPLHSGS
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                                                                                                          PSVEPVKSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 AA;
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GSSSNEPSSD SLSSPTLLAL
                                                                                                                                                                                                                 LIDILQAEID
                                                                                                                                                                                                                                                                   VVKTMTGGRA
                                                     LGMGPMATEL
                                                                                                                                                            GFPEEMSVAS
                                                                                                          SMELKTEPFD
                                                                                                                                                                                                                                                                                                                                                                                                                               February 14, 2000 08:02 Type: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40695 MW;
                                                  EPLCTPVVTC
                                                                                                                                                            LDLTGGLPEV
                                                                                                                                                                                                                 QLEDEKSALQ
                                                                                                                                                                                                                                                                   QSIGRRGKVE
                                                                                                                                                                                                                                                                                                                        PDLQWLVQPA LVSSVAPSQT
                                                                                                                                                                                                                                                                                                                                                                          SPAGDSLSYY HSPADSFSSM GSPVNAQDFC
                                                                                                          DFLFPASSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASIC MOTIF.
LEUCINE-ZIPPER.
; CDDAEF5C CRC32;
                                                                                                                                                                                                                 TEIANLLKEK
                                                                                                                                                                                                                                                                   QLSPEEEEKR
                                                  TPSCTAYTSS FVFTYPEADS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EREN C.
                                                                                                          DMDLSGSFYA
                                                                                                                                                                                                                    EKLEFILAAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding;
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OC OC OC OC
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                                                            _SEQUENCE 1.0

GDF8_BOVIN

O18836; O18829;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1999 (Rel. 36, Last sequence update)

15-DEC-1999 (Rel. 39, Last annotation update)

GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8)

GDF8 OR MSTN OR MH.
Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                   METAL
DISULFID
METAL
METAL
METAL
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                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOCHIM BIOPHYS. ACTA 1183:207-209(1993).

I: FUNCTION: FTR IS A (4FE-46] PROTEIN PLAYING A CENTRAL ROLE IN THE FERREDOXIN/THIOREDOXIN REGULATIORY CHAIN. IT CONVERTS AN ELECTRON SIGNAL (PHOTOREDUCED FERREDOXIN) TO A THIOL SIGNAL (REDUCED THIOREDOXIN) IN THE REGULATION OF EXPECTION OF SPECIFIC DISULFIDE GROUPS. CATALYZES THE LIGHT-DEPENDENT ACTIVATION OF SPECIFIC SUBUNIT: HETERODIMER OF SUBUNIT A (VARIABLE SUBUNIT) AND SUBUNIT B (CATALYTIC SUBUNIT).

B (CATALYTIC SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAIZEDB; 61547; Oxidoreductase;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
(EC 1.18.-.-) (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 94002243.
MARC-MARRIN S., SPIELMANN A., STUTZ E., SCHUERMANN P.;
"Cloning and sequencing of a corn (Zea mays) nuclear gene coding for "Cloning and sequencing of a corn (Zea mays) nuclear gene coding for the chloroplast specific catalytic subunit of ferredoxin-thioredoxin
                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                žea mays (Maize).
Žukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTRC_MAIZE P41347;
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                                                                                                                                                                                                                                                                                                      MISTVITTVG
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DB; 61547; -.
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93
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112
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121
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16740
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123
110
112
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                                                                                                                                                                                                                                                                                                      TATRGRPRRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4Fe-4S; Chloroplast; Transit peptide CHLOROPLAST (BY SIMILARITY). FERREDOXIN-THIOREDOXIN REDUCTASE,
                                                                                                                                                                                                                                                                                                                                                                               IRON-SULFUR (4FE-4S) (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
IRON-SULFUR (4FE-4S) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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LVKAQLWIYL RPVKTPATVF VQILRLIKPM

KDGTRYTGIR

SLKLDMNPGT

IDQFDVQRDA

SNLGIEIKAL

51

MQKLQISVYI YLFTLIVAGP SRLEAIKIQI LSKLRLETAP

VDLNENSEQK NISKDAIRQL

ENVEKEGLCN LPKAPPLLEL

ACLWRENTTS

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GDF8_BOVIN
                               DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
STRAIN=HOLSTEIN; TIS
MEDLINE; 98024153.
MCPHERRON A.C., LEE
"Double muscling in
                                                                   CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                MUSCIE GROWTH.

MUSCIE GROWTH.

INTELLIFIE LINKED (BY SIMILARITY).

I DEVELOPMENTAL STACE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.

LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM

DAY 31 UP UNTIL LATE GESTATION.

I TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT

SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES

M. SEMIMEMBRANOSUS AND M. BICEPS FEMORIS; LOW LEVELS IN OTHER

HINDLIMB MUSCLES.

IDISEASE: DEFECTS IN ORD RAE THE CAUSE OF THE DOUBLE-MUSCLE

PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE

DISEASE: DEFECTS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED

NUMBER OF MUSCULE FIBERS (HYPERTROPHY), RESULTING IN AN INCREASED

NUMBER OF MUSCULE FIBERS (HYPERTRADIA), RESULTING IN AN INCREASE IN

MUSCLE MASS OF 20-25%.
                                                                                                                                                                                                                                                                            This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAMBADUR R., SHARMA M., SMITH T.P.L., BASS J.J.;
"Mutations in myostatin (GDF8) in double-muscled Belgian Piedmontese cattle.";
Genome Res. 7:910-916(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97458167
KAMBADUR R., SHARI
"Mutations in myo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FRIESIAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT MH T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRON A.C., LEE S.-J.;
le muscling in cattle due
Natl. Acad. Sci. U.S.A. 9
    Length: 375
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281
309
313
339
47
71
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TISSUE-SKELETAL
  February 14, 2000
                             WW.
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                                                                                                BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e to mutations in the myostatin gene."; 94:12457-12461(1997).
                            F97E649A
                                                                                                                                            OWTH/DIFFERENTIATION SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MH LEU-94
MUSCLE;
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08:02 Type: P
                          N MH; PIEDMONTESE | N MH; PIEDMONTESE | N REF. 2).
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  9403
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GDF8_HUMAN Length: 375
ID GDF8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor;
SIGNAL
PROPEP
CHAIN
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EM peropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorseid an email to license@isb-sib.ch).
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Fiikarvota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDF8 OR MSTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i5-JUI-1999 (Rel. 38, Created)
15-JUI-1999 (Rel. 38, Last sequence update)
15-JUI-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8)
                                                                                                                                                                                                  151
                                                                                                                                                                                                                                      101
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS002
PFAM; PF00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF019627; AAB86694.1; -. MIM; 601788; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 98024153.

MCPHERRON A.C., LEE S.-J.;

"Double muscling in cattle due to mutations in the myostatin gene.";

"Double muscling in cattle due to mutations in the myostatin gene.";

Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                    351
                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY). SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYFNGEGQII YGKIPAMVVD RCGCS
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                                                  LYFNGKEQII YGKIPAMVVD
                                                                                        PKRYKANYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00250; TGF_BETA; 1.
00019; TGF-beta; 1.
actor; Cytokine; Glycoprotein; Signal.
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281
309
313
339
71
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                                                                                                                                                                 VLQNWLKQPE
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                                                                                        GECEFVFLQK
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375
372
374
339
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                                                                                                                                                                                                                                                                                                                                                                                    42750 MW;
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                                                                                                                                                                                                     VQILRLIKPM
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GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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    PRT;
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                                                                                                                               CCRYPLTVDF
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                                                                                                                                                                                                       SLKLDMNPGI
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                                                                                                                               EAFGWDWIIA
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GDF8_MOUSE
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Regulation of skeletal muscle mass in mice by a new TGF-beta superfamily member.";
Nature 387:88-90(1997).
                                                                                                                                                                                                                                                                                                                                             growth factor; Cytokine;
SIGNAL

1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinform
the European Bioinformatics Institute,
use by non-profit institutions as lone
modified and this statement is not remove
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-: TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND AD

-: TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND AD

-: SKELETAL MUSCLE, WEAK EXPRESSED IN ADIPOSE TISSUE

-: DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN

ONE-THIRD OF DEVELOPING SOMITIES. AT LATER STAGES OF DEVELOPMENT,

DETECTED IN A WIDE BANGE OF DEVELOPING MUSCLES. EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                             EMBL; U84005; AAC53167.1; -.
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351
                         301
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                                                                                                                                                                                                                                         SEQUENCE
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MLYFNGKEQI
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                          APKRYKANYC
                                                     NPELEVKVTD
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etazoa; Chordata; Craniata; Vertebrata;
dentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                          AA;
                                                   TPKRSRRDFG
                                                                                                          LRPVKTPTTV
                                                                                                                                   DYHATTETII
                                                                                                                                                            ILSKLRLETA PNISKDAIRQ LLPRAPPLRE LIDQYDVQRD
                                                                                                                                                                                                                               267
376
341
373
375
340
72
42921 MW;
IYGKIPAMVV
                          SCECEFVFLO
                                                                               TVLQNWLKQP
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 DRCGCS
                          KYPHTHLVHQ
                                                      LDCDEHSTES
                                                                                 ESNLGIEIKA
                                                                                                          FVQILRLIKP
                                                                                                                                   TMPTESDFLM
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GROWTH/DIFFERENTIATION F
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                             ANPRGSAGPC
                                                      RCCRYPLTVD FEAFGWDWII
                                                                                 LDENGHDLAV
                                                                                                           MKDGTRYTGI
                                                                                                                                     QADGKPKCCF
                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                 Type: P Check:
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                             CTPTKMSPIN
                                                                                  TEPGPGEDGL
                                                                                                           RSLKLDMSPG
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ID GDF8_PAPHA

STANDARD;

PRT;

375

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OCCUPATO
                                                                                                                             ID GDF8_PIG
AC 018831;
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Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-SKELETAL MUSCLE;

MEDLINE; 98024153.

MCPHERON A.C., LEE S.-J.;

MCPHERON A.C., LEE S.-J.;

MCPHERON A.C., LEE S.-J.;

PTOC. Natl. Acad. Sci. U.S.A. 94.12457-12461(1997).

-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SK.

MUSCLE GROWTH.

MUSCLE GROWTH.

-!- SUBURIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

-!- SUBURIT: BELONGS TO THE TGF-BETA FAMILY.

-!- SUBURIT: BELONGS TO THE TGF-BETA FAMILY.
                                                        GDF8
                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
GROWIH/DIFFERENTIATION FACTOR 8 PRECURSOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O18828;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GDF8 OR MSTN.
Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammmalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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                                                                                                                                                                                                                                                                                                                                                                  51
                                                        OR MSTN
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 375
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281
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71
                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                      VQILRLIKPM
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POTENTIAL.
61C8D2B7 CRC32;
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GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY.
                                                                                                                                         PRT;
                                                                PRECURSOR (GDF-8)
                                                                                                                                         375
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                                                                                                                                                                                                                                                                       DENGHDLAVT
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                                                                (MYOSTATIN)
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IIAA_SEQUENCE 1.0
ID GDF8_RAT
AC 035312;
DT 15-JUL-1999 (F
DT 15-JUL-1999 (F
DT 15-JUL-1999 (F
DE GROWTH/DIFFERE
GN GDF8 OR MSIN.
OS RATTUS NOTVO95)
OC EUKARYOTA; Met
OC EUKARYOTA; Met
OC EUKARYOTA; Met
OC TISSUE=SKELET/
                                                                                                                                                                                                                                                                                                                                                                                                                                              GDF8_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 98024153.
MCPHERRON A.C., LEE S.-J.;
MCPHERRON A.C., LEE S.-J.;
Pouble muscling in cattle due to mutations in the myostatin Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF019623; AAB86690.1; -
EMBL; AF033855; AAC08035.1; -
EMBL; AF033855; AAC08035.1; -
EMBL; AF093798; AAC62489.1; -
PROSITE; PS00250; TGF_BETA; 1.
PFAN; PF00019; TGF_BETA; 1.
PFAN; PF00019; TGF_BETA; 1.
PFAN; PF00019; TGF_BETA; 1.
POTENTIAL.
POTENTIAL.
                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8)
GDF8 OR MSIN.
SEQUENCE FROM N.A.
TISSUE=SKELETAL MUSCLE;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor;
SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUSCLE GROWTH.
-!- SUBCURIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        51
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milted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF
                                                                                                                                                                                                                    LYFNGKEQII YGKIPAMVVD
                                                                                                                                                                                                                                               PKRYKANYCS
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375
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GROWPH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                               (MYOSTATIN)
                                            Mammalia;
Rattus.
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SETTITITION OF THE PROPERTY OF
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Eutheria; Cetari
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation (Applease)
GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN)
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**POUDLE muscling in cattle due to mutations in the myostatin gene.";

**POC. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

-i- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
                                                                                                        "Double mus
Proc. Natl.
                                                                                                                                                                                                                                                       Caprinae;
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SUBUNIT: HOMODINER, DISULFIDE-LINKED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                 SUBUNIT: HOMODIMER, SIMILARITY: BELONGS
                                                                            uble muscling in cattle due to mutations in the myostatin c. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997). EUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SI
                                                             MUSCLE GROWTH.
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N A.C., L
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); TGF-beta; 1.
; Cytokine; Glycopr
                                                                                                                                                  , LEE S.-J
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376
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                 DISULFIDE-LINKED (BY SIMILARITY).
TO THE TGF-BETA FAMILY.
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Glycoprotein;
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GROWNH/DIFFERENTIATION FACTOR 8
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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Pecora; Bovoidea; Bovidae;
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                                                                                      SKELETAL
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GDF8_SHEEP
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01-NOV-1997
15-JUL-1999
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 96029146.
HUANG C.H., XIE S.S., SOCHA W., BLUMENFELD O.O.;
"Sequence diversification and exon inactivation in the g
gene family from chimpanzee to human.";
J. MOI. EVOL. 41:478-486(1995).
- FUNCTION: THIS PROTEIN IS A MINOR SIALOGLYCOPROTEIN
MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00250; PFAM; PF00019; TGF-beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, C)
01-NOV-1997 (Rel. 35, La
15-JUL-1999 (Rel. 38, La
GLYCOPHORIN B PRECURSOR.
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                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                 GYPB OR GPB
                                                                                                                                                                                                                                                                                                                                                                                GLPB_PANTR
Q28914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                            This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst between Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                            -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE GLYCOPHORIN A FAMILY.
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TE; PS00250;
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0; TGF_BETA; 1.
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35, Last sequence update)
38, Last annotation updat
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPTESDLLAE VQEKPKCCFF
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GROWTH/DIFFERENTIATION FACTOR
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
B36084EE CRC32;
                                                                                                                                                                                                                                                                           Craniata; Vertebrata; i; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                             123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DENGHDLAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDGTRYTGIR
                                     (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                                                                                                        Mammalia;
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GPDA_ECOLI
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                                                                                                                                                                                                                  Oxidoreductase; NAD. SEQUENCE 339 AA;
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or or send an email to license@isb-sib.ch).
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFIA H.J., BURLAND V., DANIELS D.L., PLUNKETT G. III, BLATTNER F. "ANALYSIS Of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes", Nucleic Acids Res. 22:2576-2586(1994).

-!- CATALYTIC ACTIVITY: SN-GLYCEROL 3-PHOSPHATE + NAD(+) -

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

-!- SUBCELLULAR LOCATION: OTHE NAD-DEPENDENT GLYCEROL-3-PHOSPHATE
                                                                                                                                                                                                                                        ECOGENE; EG20091; GPSA.
PROSITE; PS00957; NAD_G3PDH;
PFAM; PF01210; NAD_G1Y3P_dh;
                                                                                                                                                                                                                                                                                  EMBL; U00039; CAB34639.1; -.
EMBL; AE000439; AAC76632.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] (EC 1.1.1.8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-K12 / MG1655;
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PROSITE; PS00312; GLYCOPHORIN_A; 1.
PFMM; PF01102; Glycophorin_A; 1.
Erythrocyte; Transmembrane; Sialic
                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia.
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GVEMPITEEI YQVLYCGKNA REAALTLLGR ARKDERSSH
                          LTCTDNQSRN RRFGMMLGQG
                                                    GAGMSDGIGF
                                                                                                                                                              MNQRNASMTV
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                                                    GANARTALIT
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113 P
13246 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
                                                                                                                                  TALAASRNIL VVVPSHVFGE VLRQIKPLMR
                                                                                                                                                           AITLARNGHE VVLWGHDPEH IATLERDRCN
                        MDVQSAQEKI GQVVEGYRNT
                                                    RGLAEMSRLG
                                                                               LHCGKSFRVY
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BY SIMILARITY.
GLYCOPHORIN B.
POTENTIAL.
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                                                                             SNPDFIGVQL
                                                                                                        QIPLAVISGP
                                                   AALGADPATF
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GPRD_HUMAN
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                                                                                                                                                                                                          EMBL; U20350; AAA917
EMBL; U28934; AAA870
GCRDB; GCR_1992; --
GCRDB; GCR_2014; --
MIM; 661470; --
PROSITE; PS00237; G_
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 96011651.

RAPORT C.J., SCHWEICKART V.L., EI

RAPORT C.J., SCHWEICKART V.L., EI

"The orphan G-protein-coupled rec

related to genes for chemokine re
and neural tissues.";

Gene 163:295-299(1995).
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DISULFID
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                     SEQUENCE
                                                                                                             TRANSMEM
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 95374679.
                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR13 (V28) (BETA CHEMOKINE RECEPTOR-LIKE 1) (CMK-BRL-1) (CMKBLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3PRD_HUMAN
 Length:
                                                                                                                                                                                                PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                       coupled
                     355
                                       AAA91783.1;
AAA87032.1;
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                                                          February 14,
                     40396
                     MW;
                                                                                                           3 (POTENTIAL).
CYTOPLASMIC (P.
                                                                                                                                                                                      Transmembrane
                   CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
; E809E31D CRC32;
                                                                     CYTOPLASMIC
6 (POTENTIA
                                                                                                                              2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL)
                                                    EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
                                                                                          EXTRACELLULAR (POTENTIAL 5 (POTENTIAL).
                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , EDDY R.L. JR., SHOWS T.B., GRAY P.W.; receptor-encoding gene V28 is closely e receptors and is expressed in lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Mammalia; i; Hominidae; Homo.
                                                  (POTENTIAL)
                                                                     (POTENTIAL
                                                                                       (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                            (POTENTIAL).
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Type: P
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MDQFPESVTE

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LVVFALTNSK KPKSVTDIYL LNLALSDLLF VATLPFWTHY LINEKGLHNA

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LLVVLALTNS

RKSKSITDIY FIGFFGGIFF

LLNLALSDLL

FVATLPFWTH YLISHEGLHN

151

SIGVWAAAIL

VASPQFMFTK

RKDNECLGDY

PEVLQEIWPV LRNSEVNILG

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GPRD_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE; 94323113.
HARRISON J.K., BARBER C.M., LYNCH K.R.;
"CDNA clonding of a G-protein-coupled receptor cord and brain related to chemokine receptors. Neurosci. Lett. 169.85-89(1994).
-i- FUNCTION: ORPHAN RECEPTOR. COULD BE A CHEMOTE COURT OF THE PROPERSION COULD BE A CHEMOTE COURT OF THE PROPERSION COULD BE A CHEMOTE COURT OF THE PROPERSION COULD BE A CHEMOTE COULD BE 
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01-JUN-1994 (Rel. 29, Last seq
01-WOV-1997 (Rel. 35, Last ann
01-WOV-1997 (Rel. 35, Last ann
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
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DOMAIN
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GCRDB; GCR_0268; -.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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STRAIN-SPRAGUE-DAV
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00001;
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TISSUE SPECIFICITY: MOST ABUNDANT IN ADULT SPINAL CORD, E
KIDNEY, GUT, UTERUS AND TESTES.
PTM: THIS PROTEIN IS NOT N-CLYCOSYLATED WHICH IS UNUSUAL
G-PROTEIN-COUPLED RECEPTORS.
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annotation update)
RECEPTOR GPR13 (RBS11).
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   14,
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CYTOPLASMIC (POTENTIAL)
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BY SIMILARI
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
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5 (POTENTIAL)
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GRAB_MOUSE P04187;
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20-MAR-1987 (Rel. 04, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
15-RANZYME B(G, H) PRECURSOR (EC 3.4.21.79) (CYTOTOXIC CELL PROTEASE (CCEL) (CTLA-1) (FRAGMENTIN 2).
GZMB OR CTLA-1 (OR CTLA-1.2).
                                                                                                                                                                                                                                                                                 BRUNET J. P. DOSSETO M., DENIZOT F., MATTEI M.-G., CLARK W.R., HAQQI T.M., FERRIER P., NABHOLZ M., SCHMITT-VERHULST A.M., LUCIANI M.F., GOLSTEIN P.;
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE; 86284960.
BRUNET J.F., DOSSETO M.,
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE: 8905244.

LOBE C.G., UPTON C., DUGGAN B., EHRMAN N., LET

MCFADDEN G., BLEACKLEY R.C.;

"Organization of two genes encoding cytotoxic

serine proteases CCPI and CCPII.";

Biochemistry 27:6941-6946(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                               MEDLINE; 94319082.

KO M.S., WANG X., HORTON J.H., HAGE MAEZAKI Y., NADEAU J.H.;

"Genetic mapping of 40 cDNA clones Mamm. Genome 5:349-355(1994).
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3D-STRUCTURE MODELING.
MEDLINE: 89164501.
MURCHY M.E.P. MOULT J., BLEACKLEY R.C.,
MURCHY M.E.P. MOULT J., BLEACKLEY R.C.,
WELSSMAN I.L., JAMES M.N.G.;
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cytotoxic T lymphocytes.";
                                                                                                                SEQUENCE OF 21-40.
MEDLINE; 87215932.
MASSON D., TSCHOPP J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 86208120.

LOBE C.G., FINLAY B.B., PARANCHYCH
NOVEL serine proteases encoded by
Lymphocyte-specific genes.";
science 232:858-861(1986).
                                                                                                                                                                                                                                                           EQUENCE OF 227-247 FROM N.A.
                                                                                         lī 49:679-685(1987).
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Mus.
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01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
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EMBL; M12302; AAA37383.1; -
EMBL; M25256; AAB61756.1; -
EMBL; U05707; AAB60470.1; -
PIR; A00956; PRMSCL.
PIR; A28952; A28952.
PIR; B26944; B26944.
PDB; 2CP1; 15-OCT-94.
                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
7-ALPHA-HYDROXYSTEROID DEHYDROGENASE (EC 1.1.1.159)
7-DEHYDROXYLASE) (7-ALPHA-HSDH).
Clostridium sordellii.
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CARBOHYD
SEQUENCE
7-DEHILL
Clostridium solu-
Clo
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PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license(sb-sb-ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis;
SIGNAL
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CASPASE-3, -7, -9 AND 10 TO GIVE RISE TO ACTIVE ENZYMES ME
APOPTOSIS (BY SIMILARITY).
CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ASP-|-XAA >> AS
> MET-|-XAA, SER-|-XAA.
SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF CYTOLYTIC T-
LYMPHOCYTES AND NATURAL KILLER CELLS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
TRYDSIN FAMILY. STRONGEST TO OTHER GRANZYMES AND TO MAST C
PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tedins 4:190-204(1988).

FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-MEDIATED INMUNE RESPONSES. IT CLEAVES AFTER ASP. SEEMS TO BE LINKED TO AN ACTIVATION CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES CASPASE-3, -7, -9 AND 10' TO GIVE RISE TO ACTIVE ENZYMES MEDIATING CASPASE-3, -7, -9 AND 10' TO GIVE RISE TO ACTIVE ENZYMES MEDIATING
                                                                                                                                                                                                                                                                                                 GDSGGPLVCK KVAAGIVSYG
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27470 MW;
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                    Bacillus/Clostridium
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A EMBL; L12058; AAA53556.1; -.

R HSSP; p25529; lAHH.

DR PROSITE; P2500061; ADH_SHORT; 1.

DR PFAM; PF00106; adh_Short; 1.

DR PFAM; PF00178; adh_Short; 2:

DR Oxidoreductase; NADP; Bile acid catabolism.

KW Oxidoreductase; NADP; Bile acid catabolism.

NO BIND 10 34 BY SIMILARITY).

158 158 BY SIMILARITY).

Type: I
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  SEQUENCE FROM N.A.
MEDIJNE: 84207945.
STRUBIN M., MACH B., LONG
"The complete sequence of
invariant chain reveals a
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 86093681.
KUDO J. CHAO L.Y., NARNI F., SAUNDERS (
"Structure of the human gene encoding to 
class II histocompatibility antigens."; 
Nucleic Acids Res. 13:8827-8841(1985).
[2]
                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                                                                                                                                                                                                                           P04233; Q29832;
20-MAR-1987 (Rel. 04, Created)
01-JUL-1933 (Rel. 26, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CH
ASSOCIATED INVARIANT CHAIN) (P33) (CD74 ANTIGEN).
CD74 OR DHLAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 1.0
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-!- INDUCTION: BY BILE ACID. EXPRESSED DURING GROWTH-PHASE.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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polypeptide with
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HLA-DR-associated an unusual transmembrane
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CLAESSON L., LARHAMMAR D., RASK L., PETERSON P.A.; "CDNA clone for the human invariant gamma chain of clhistocompatibility antigens and its implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JASANOFE A. WAGNER G., WILEY D.C.;

JASANOFE A. WAGNER G., WILEY D.C.;

Structure of a trimeric domain of the MHC class II-associated chaperonin and targeting protein II.";

EMBO J. 17.6812-6818(1998).

- PUNCTION: PLAYS A CRITICAL ROLE IN MHC CLASS II ANTIGEN PROCESSING PRONCISION.

- PUNCTION: PLAYS A CRITICAL ROLE IN MHC CLASS II ANTIGEN PROCESSING COMPLEX SOON AFTER THEIR SYNTHESIS AND DIRECTING TRANSPORT OF THE COMPLEX FROM THE ENDOPLASMIC RETICULUM TO COMPARTMENIS WHERE PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II TAKES PLACE.

- PEPTIDE LOADING OF CLASS II THE ALPHA, BETA/GAMMA HETEROTRIMERS.

- SUBUNIT: NONAMER COMPOSED OF THEE ALPHA, BETA/GAMMA HETEROTRIMERS.

- SUBUNIT: NONAMER COMPOSED OF THEE ALPHA, BETA/GAMMA HETEROTRIMERS.

- SIMILARITY: CONTAINS I THYROGLOBULIN TYPE-I DOMAIN.

- SIMILARITY: CONTAINS I THYROGLOBULIN TYPE-I DOMAIN.

- PATABASE: NAME-PROW; NOTE-CD Guide CD74 entry.

- WWM-"http://www.ncbi.nlm.nih.gov/prow/cd/cd71.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polarity.";
EMBO J. 3:869-872(1984).
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Proc. Natl.
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GHOSH P., AMAYA M., MELLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 134-208.
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                                                              DOMAIN
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                        PROSITE; PS00484; THYROGLOBULIN_1; 1.

PFAM; PF00086; thyroglobulin_1; 1.

Glycoprotein; MHC; Proteoglycan; Transmembrane; Alternative
                                                                                                                                                                                                                                                         EMBL; X03339; CAA27046.1; -.
EMBL; X03340; CAA27047.1; -.
EMBL; K01144; AAA36304.1; -.
EMBL; X00497; CAA25192.1; -.
EMBL; X00497; CAA25193.1; -.
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                                                                                                                                                                                                            A30060; HLHUG.
1A6A; 27-MAY-98.
1IIE; 15-FEB-99.
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                                                                                                                                3D-structure
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                                                                CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMERANE
EXTRACELLULAR (POTENTIAL).
CLIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83:4484-4488(1986).
 GLYCOSAMINOGLYCAN. THYROGLOBULIN TYPE
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                                                                                                                                                                                     EMBL; X13464; CAA31824.1; -. EMBL; J01804; AAA88616.1; -. PIR; JS0158; XNEBHC.
                                                                                          Histidine
Pyridoxal
BINDING
                                                                                                                                        STYGENE; SG10159; HISC.
PROSITE; PS00599; AA_TRANSFER_CLASS_2;
PFAM; PF00222; aminotran_2; 1.
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y; pr00222; aminorian, tidine biosynthesis; 'idoxal phosphate: 17 217 217 164

Transferase; Aminotransferase;

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217 164

PYRIDOXAL PHOSPHATE (F DGTRVVFVCSPNNPTGQ -> T (IN REF. 2). C -> R (IN REF. 1). L -> S (IN REF. 1). GI -> ES (IN REF. 1).

(PROBABLE). > TAQKWCSFVAPIILPDN

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I IAA SEQUENCE 1
ID HIS8_SAITY
AC P10369;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BARNES W.M., HUSSON R.N., WHITTIER R.;

SUBMILTED (AUG-1989) to the EMBL/GenBank/DDBJ databases.

SUBMILTED (ACTIVITY: L-HISTIDINOL-PHOSPHATE + 2-OXOGLUTARATE = 3-(IMIDAZOL-4-YL)-2-OXOFROPYL PHOSPHATE + GLUTAMATE.

-!- COFACTOR: PYRIDOXAL PHOSPHATE.

-!- SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.
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MEDITIVE: 8094829.

CARLONAGNO M.S., CHIARIOTTI L., ALIFANO P., NAPPO A.G., BRUNI C.B.;

CSTRUCTURE and function of the Salmonella typhimurium and Escherich

coli K-12 histidine operons.";

J. Mol. Biol. 203:585-606(1988).
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01-AUG-1992 (Rel. 23, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9) (IMIDAZOLE ACETOL-
PHOSPHATE TRANSAMINASE).
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                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Bacteria; Proteobacteria;
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDIINE; 97426617.

BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BUBLATINER F.R., PLOLLABO-VIDES J., GLASNER F.D., RODE C.K., MAYHI GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSI MAU B., SHAO Y.;

MAU B., SHAO Y.;

"The complete genome sequence of Escherichia coli K-12.";

science 277:1453-1474(1997).
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Submitted (JAN-1996)
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S J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
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annotation update)
PERMEASE PROTEIN HISQ
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HISQ_ECOLI Length: 228
                                                                                                 "PCR cloning expressed in
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE, 93087175.
CROMPTON N.R., BARTLETT T.J., MACGREGOR A.D., MANFIOLETTI BURATTI E., GLANCOTTI V., GOODWIN G.H.;
BURATTI E., GLANCOTTI V., GOODWIN G.H.;
TIDENTIFICATION OF A novel vertebrate homeobox gene expressible mematopoletic cells."
haematopoletic cells."
haematopoletic cells."
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Acids Res. 20:5661-5667(1992).
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PRHX OR PRH OR HEX.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
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TRANSMEM
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TRANSMEM
MEDLINE, 93219088.
BEDFORD F.K., ASHWORTH A., ENVER T., W
BEDFORD F.K., ASHWORTH A., ENVER T., W
THEX: a novel homeobox gene expressed
conserved between mouse and human.";
Nucleic Acids Res. 21:1245-1249(1993).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 32, Last annotation update)
01-WOV-1995 (Rel. 32, Last annotation update)
HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX).
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EMBL; D47023; AAC75368.1; -.
EMBL; D90862; CAB22089.1; -.
ECOGENE; EG12125; HISO.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
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                                                                   EQUENCE OF 122-270 FROM N.A.
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                                                                                          Biophys.
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                                                                                       COLLINS S.J., RADICH J.; of an orphan homeobox gene (PRH) preferentially myeloid and liver cells."; phys. Res. Commun. 195:976-983(1993).
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periplasmic (POTENTIAL).
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V -> C (IN R)
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W (IN REF. 1).
W (IN REF. 1).
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                                                         SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-EMBRYO;

STRAIN-C59BL/6J; TISSUE-EMBRYO;

MEDLINE; 9321908.

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SEQUENCE
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EMBL; L16499; AAA02998.1; -.
EMBL; Z1533; CAA79730.1; -.
EMBL; S26799; S26799.
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN
PRHX OR HHEX.
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FUNCTION: RECOGNIZES THE DNA SEQUENCE 5'-ATTAA-3'. MAY PLATING THE MATOPOLETIC DIFFERENTIATION.
SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
TISSUB SPECIFICITY: LIVER AND PROMYELOCYTIC LEUKEMIA CELLLINE HL60.
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DNA-binding; Developmental
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345:93-88(1994).
N: RECOGNITATION
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115 L -> V (IN REF. 2).
30021 MW; 453E9E6A CRC32;
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    DURING H
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d during haematopoiesis
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    HEMATOPOIESIS
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HMPH_MOUSE
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HPRK_BACSU
034483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Bactilus subtilis.
Bactilus Firmicutes; Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Bacillus.
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SEQUENCE
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                                                                                                                                                                                                                                                 MEDLINE; 98230327.

REIZER J., HOTSCHEN C., TITGEMEYER F., RIVOLTA C., STUELKE J., KARAMATA D., SAIER M.H. JR., HILLEN W.; A novel protein kinase that controls carbon catabonarteria.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
LAZAREVIC V., SOLDO B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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PROSITE; PS00027; HOMEOBOX_1;
PROSITE; PS50071; HOMEOBOX_2;
PFAM; PF00046; homeobox; 1.
                                                                                                                      MEDLINE; 99141583.

MEDLINE; 99141583.

KRAVANJA M., ENGELMANN R., DOSSONNET V., BLUGGEL M., MEYER H.E.,

FRANK R., GALINIER A., DEUTSCHER J., SCHNELL N., HENGSTENBERG W.;

The hprk gene of Enterococcus faecalis encodes a novel bifunctional

"The upp kinase/phosphatase.";
                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, MEDLINE; 98230327
                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HPR(SER) KINASE/PHOSPHATASE (EC 2.7.1.-) (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homeobox; DNA-binding; Developmental DOMAIN 1 134 PRO-RICI DOMA_BIND 138 197 HOMEOBO
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                                                                                                                                                                                                                                                                                                                                                                                   KARAMATA D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                         CHARACTERIZATION OF THE PHOSPHATASE ACTIVITY
                                                                                                                                                                                                                                        Microbiol.
TYME: the HPT kinase/phosphatase.";

(. Microbiol. 31:59-56(1999).

FUNCTION: THIS KINASE/PHOSPHATASE REGULATES CARBOHYDRATE UPTAKE AND METABOLISM BY PHOSPHORYLATING/DEPHOSPHORYLATING SER-45 OF THE PHOSPHORYL CARRIER PROTEIN (HPR) OF THE PHOSPHORYLATE DEPENDENT SUGAR PHOSPHOTRANSPERASE SYSTEM (PTS) IN RESPONSE TO CYTOPLASMIC METABOLITE LEVELS AS A DEVICE FOR THE MODULATION OF CARBON CARBON CARBON CARBON CARBON CARBON CARBON CALCULATION: ALLOSTERICALLY ACTIVATED BY METAPOLITE REPESSION.
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271 AA;
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HUPK_RHILV
P28153;
                                                                       SEQUENCE FRO
                              SCHMITT
TICHY H.
                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE; 95020662.

IMPERIAL J., REY L., RUIZ-ARGUESO T.;

"Hupk, a hydrogenase-ancillary protein from Rhizobium leguminosarum,
shares structural motifs with the large subunit of NiFe hydrogenases
and could be a scaffolding protein for hydrogenase metal cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                          MEDILINE; 93108466.

REY L., HIDALGO E., PALACIOS J.M., RUIZ-ARGUESO T.;

"Nucleotide sequence and organization of an H2-uptake gene cluster from Rhizobium leguminosarum bv. viciae containing a rubredoxin-like gene and four additional open reading frames.";

J. Mol. Biol. 228:998-1002(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-128C53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium leguminosarum (biovar
Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
01-WOV-1997 (Rel. 35, Last annotation HUPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
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NP_BIND
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EMBL; Z99121; CAB15505.1; -.
SUBTILIST; BG14125; PTSK
Multifunctional enzyme; Transferase; Serine/threonine-protein
ATP-binding; Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIEDGEQEE
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                                                 H.,
                                                                                                   FROM N.A.
LOTZ W.;
(SEP-1994) to
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152
309 AA;
                                                 KOKOTEK W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium.
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159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34571 MW;
  the EMBL/GenBank/DDBJ databases
                                                    THUERING
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SEQUENCE FROM N.A.

CONTRAINERS 97426617.

BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,

BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,

RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,

AND ALL SHAO Y.,

BANGUR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,

AND ALL SHAO Y.,

The complete genome sequence of Escherichia coli K-12.",

CIECTRON COMPLETE GENOREM METABOLISM; FHL PATHWAY.

CIECTRON CORNERIORS AND A HYDROGENASE, UNIDENTIFIED ELECTRON CARRIERS AND A HYDROGENASE (ISOENZYME 3). IN THIS NON-

ENERGY CONSERVING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM FORMATE ARE RELEASED.

CIECTRON CONSERVING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM FORMATE ARE RELEASED.

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CIECTRON STATING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM FORMATE BELONGS TO THE COMPLEX I SUBUNIT I FAMILY.
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Escherichia co
Bacteria; Pro
Escherichia.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.;
STRAIN-K12 / MC4100;
MEDLINE; 90251163.
BOEHM R., SAUTER M., BOECK A.;
"Nucleotide sequence and expression of an operon coding for formate hydrogenlyase components.";
Mol. Microbiol. 4:231-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16430;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
FORMATE HYDROGENLYASE SUBUNIT 4 (FHL SUBUNIT COMPONENT D).
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PROSITE; PS00667;
PROSITE; PS00668;
PFAN; PF00146; NI
OXIGOTEDUCTASE;
TRANSMEM 68
TRANSMEM 94
TRANSMEM 168
TRANSMEM 168
TRANSMEM 222
TRANSMEM 222
TRANSMEM 222
TRANSMEM 225
SEQUENCE 307 AJ
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MADDA K., WAKABAYASHI S., MATSUBARA H.;

MAEDA K., WAKABAYASHI S., MATSUBARA H.;

MAEDA K., WAKABAYASHI S., MATSUBARA H.;

MAEDA M.;

MATSUBARA H.;

MATSUBARA H.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ALPHA-AMYLASE INHIBITOR 0.19 (0.19 AI) (0.19 ALPHA-AI).
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
roaceae; Triticum.
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                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-KERNEL; OKUDA M., SATOH T.
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                                                                                                                                               OKUDA M., SATOH T., SAKURAI N., SHIBUYA K., KAJI H., SAMEJIMA "Overexpression in Escherichia coli of chemically synthesized active 0.19 alpha-amylase inhibitor from wheat kernel."; J. Biochem. 122:918-926(1997).
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MEDLINE: 98022743.

ODA Y., MATSUNAGA T., FUKUYAMA K., MIYAZAKI T., MORIMOTO T.;

"Tertiary and quaternary structures of 0.19 alpha-amylase inhibitor

from wheat kernel determined by X-ray analysis at 2.06-A

resolution.";
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IIAA_SEQUENCE 1.0
IID INA2_WHEAT
AC POIO83;
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DT 21-JUI-1986 (F
DT 01-JUN-1994 (F
DT 01-JUN-1
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RC STRAIN-CV. PA
RX MEDLINE; 9133
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RA GARCIA-MAROTC
RT WAAI-1, a whe
RL PLANT NO. BI
CC -i- SUBUNIT:
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   MEDLINE; 92032760.

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

GARCIA-MAROTO F., CARBONERO P., GARCIA-OLMEDO F.;

TISCUE NIL MUNICALE INTERPALAMINATION PROMER.

-!- SUBUNIT: MONOMER.

-!- TISSUE SPECIFICITY: ENDOSPERM.
                                                                                                                                             POERIO E., CAPORALE C., CARRANO L., PUCCI P., BUONOCORE V.;
"Assignment of the five disulfide bridges in an alpha-amylase
inhibitor from wheat kernel by fast-atom-bombardment mass
spectrometry and Edman degradation.";
Eur. J. Blochem. 199:595-600(1991).
                                                                                                                                                                                                                                                                                             SEQUENCE.

KASHLAN N., RICHARDSON M.

"The complete amino acid
of alpha-amylase.";
                                                                                                                                                                                                                                                                                                                                                                       ALPHA-AMYLASE INHIBITOR 0.28 (CIII) (WMAI-1).

Trittcum aestivum (Wheat).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; Lillopsida; Poales;

Poaceae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
ALPHA-AMYLASE INHIBITOR 0.28 (CIII) (WMAI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
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MEDLINE; 91330910.
POERIO E., CAPORALE C.,
                                                                                                                                                                                                                                                                      Phytochemistry
[2]
                                                                                                                                                                                                                                                      SEQUENCE, AND DISULFIDE
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13337 MW; 05CA1F5D.CRC32;
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PIR; ---

WIWTA.

PTM: THE DISULFIDE BONDS ARE ESSENTIAL FOR THE INHIBITOR ACTIVITY SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR FAMILY.

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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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PIR; A01323; WIWITAS.

HSSP; P01085; 1HSS.
PROSITE; PS00426; CEREAL_TRYP_AMYL_INH; 1.
PFAM; PF00234; tryp_alpha_amyl; 1.
Alpha-amylase inhibitor; Multigene family; S
DISULFID 20 41 OR 20-42.
DISULFID 20 83
DISULFID 42 99 OR 41-99.
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PFAM; PF00234; tryp_alpha_amyl; 1.
Alpha-amylase inhibitor; Multigene family;
DISULFID 7
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REVISIONS TO 119-124.

MEDLINE; 85175148.

MAEDL K., WARKBAYASHI S., MATSUBARA H.;

"Complete amino acid sequence of an alpha-amylase kernel (0.19-inhibitor).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 83127436.
MAEDA K., HASE T., MATSUBARA H.;
"Complete amino acid sequence of an alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Triticum.
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21-JUL-1986 (Rel. 01, Last sequence up
01-JUN-1994 (Rel. 29, Last annotation
ALPHA-AMYLASE INHIBITOR 0.53.
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Y -> A (IN VERY SMALL AMOUNT).
CK -> GP (IN VERY SMALL AMOUNT).
A -> C (IN REF. 1).
82F56DD7 CRC32;
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CASPASE-2 SUBUNIT 1 CASPASE-2 SUBUNIT 2 BY SIMILARITY.

(BY (BY

SIMILARITY).

Hydrolase;

protease; 266 >312 210

Apoptosis;

Zymogen.

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                                                                                                                        PFAM;
PFAM;
PFAM;
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HIRSHFIELD A.N., TILLY J.L.;

Interleukin-1 beta-converting enzyme-related proteases (IRPS) and mammalian cell death: dissociation of IRP-induced oligonucleosomal mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle.",

Endocrinology 136:5042-5053(1995).

FINCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

-I- FUNCTION: INVOLVED IN THE ACTIVATION. MIGHT FUNCTION BY EITHER ACTIVATING SOME PROTEINS REQUIRED FOR CELL DEATH OR INACTIVATING PROTEINS NECESSARY FOR CELL SURVIVAL (BY SIMILARITY).

SUBULILY HETERODIMER OF A SMALL AND A LARGE SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a obetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or.sed an email to license@isb-sib.ch).
                                                                                                                                                                                                         EMBL; AF025671; AAB82567.1; -.
EMBL; U34684; AAC52260.1; -.
HSSP; P29466; IIBC.
PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS01122; CASPASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-KIDNEY CORTEX;

MEDLINE; 98191309.

KAUSHAL 6.P., SINGH A.B., SHAH S.V.;

KAUSHAL 6.P., SINGH A.B., SHAH S.V.;

"Identification of gene family of caspases in expression in ischemia reperfusion injury.";

Am. J. Physiol. 274:F587-F595(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
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Eutheria; Rodentia;
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SIMILARITY: BELONGS TO PERTIDASE FAMILY C14; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASPASE FAMILY.
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PF00655; ICE_P10;
PF00656; ICE_P20;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 94122379.
HABU Y., SAKATA Y., FUKASAWA K., OHNO T.;
"Ubiquitous nuclear proteins bind to 5' upstream rounitz chymotrypsin inhibitor gene in winged bean.
Kunitz chymotrypsin inhibitor 1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
01-JUL-1991 (Rel. 19, Last sequence update)
10-JUL-1992 (Rel. 38, Last annotation update)
15-JUL-1992 (Rel. 19, Last sequence)
15
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-207.

MEDLINE; 89197853.

SHIBATA H., HARA S., IKENAKA T.;

"Amino acid sequence of winged bean (Psophocarpus tetragonolobus DC.) chymotrypsin inhibitor, WCI-3.";

DC.) chymotrypsin inhibitor, WCI-3.";

J. Biochem. 104:537-543(1988).
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HABU Y., PEYACHOKNAGUL S., UMEMOTO K., SAKATA Y., OHNO T.;
HABU Y., PEYACHOKNAGUL S., UMEMOTO K., SAKATA Y., OHNO T.;
"Structure and regulated expression of Kunitz chymotrypsin inhibitor
"Structure and regulated expression of Kunitz chymotrypsin inhibitor
genes in winged bean [Psophocarpus tetragonolobus (L.) DC.].";
genes in winged bean [Psophocarpus tetragonolobus (L.) DC.].";
J. Biochem. 111:249-258(1992).
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PEYACHOKNAGUL S., MATSUI T., SHIBATA H., HARA S., IKENAKA T.,

OKADA Y., OHNO T.;

Sequence and expression of the mRNA encoding the chymotrypsin

inhibitor in winged bean (Psophocarpus tetragonolobus (L.) DC.).";

plant Mol. Biol. 12:51-58(1989).
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   X-AAY CRYSTALLOGRAPHY
MEDLINE; 99258819.
DATTAGUPTA J.K., PODDE
DUTTA S.K., SINGH M.;
                                                                                                                                                                      "Structure of a Kunitz-Type 2.95-A resolution."; Acta Crystallogr. D 52:521-
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IDI_MYCTU

F72002; 008150;

15-DEC-1999 (Rel. 39, Created)

15-DEC-1999 (Rel. 39, Last sequence update)

15-DEC-1999 (Rel. 39, Last annotation update)

PUTATIVE ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2) (IPP ISOMERASE) (ISOPENTENYL PYROPHOSPHATE ISOMERASE).

RV1745C OR MTCY28.08C OR MTCY04C12.29C.

Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor; S
SIGNAL 1 24
CHAIN 25 207
DISULFID 65 109
DISULFID 159 168
ACT_SITE 89 90
SEQUENCE 207 AA; 22774 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
DISULFID
DISULFID
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINGH
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BL; D13974; BAA03085.1; -.
BL; D13975; BAA03085.1; -.
BL; D13976; BAA03086.1; -.
BL; D13976; BAA03086.1; -.
BC; S42563; S42563.
R; S42563; S42564.
R; S42564; S42564.
R; S42564; S42564.
B; 14WBC; 12-MBR-99.
B; 44WBC; 12-MBR-99.
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.13-A structure of a Kunitz-type winged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (OCT-1998) to the PDB data bank. FUNCTION: INHIBITS ALPHA-CHYMOTRYPSIN AT THE MOLAR RATI IN STATE OF 1:1.
SIMILARITY: TO OTHER LEGUMINOUS KUNITZ-TYPE INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SETASSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHVYKLLYCQ
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207
207
168
90
22774 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSPNEVSKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REACTIVE BOND (CHYMOTRYPSIN); 22B8B770 CRC32;
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STRAIN=H37RV;
MEDLINE; 98295987.
COLE S.T., BROSCH R., 1
GORDON S.V., EIGLMEIER

PARKHILL R K., GAS

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GARNIER BARRY C.

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CHURCHER C

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HARRIS

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!!AA_SEQUENCE 1.0
ID IDNR_ECOLI
AC P39343;
DT 01-FEB-1995 (
DT 01-FEB-1995 (
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          A LO COCCO C
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DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
HORNSBY T., JAGELS K., KROCH A., MCLEAN J., MOULE S., MURPHY L.,
OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROCERS J.,
RUTTER S., SEBGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.",
nature 393:537-544(1998).
-i- FUNCTION: CATALIZES THE 1,3-ALLYLIC REARRANGEMENT OF THE
HOMOALLYLIC SUBSTRATE ISOPENTENYL (IPP) TO ITS ALLYLIC ISOMER,
DIMETHYLALLYL DIPHOSPHATE (DMAPP) (BY SIMILARITY).
-i- CATALIZE T. SOPENTENYL DIPHOSPHATE - DIMETHYLALLYL
DIPHOSPHATE.
"Sequence analysis of the GntII (subsidiary) system for gluconate metabolism reveals a novel pathway for L-idonic acid catabolism in Escherichia coll.";

Jacteriol. 180:3704-3710(1998).

-i- FUNCTION: IDN OPERON REGULATOR. MAY REPRESS GNTKU AND GNTT GENUMEN GROWING ON L-IDONATE.
                                                                                                                                                                                   BAUSCH C.,
CONWAY T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIK-MEDITIES;
MEDITIES; 9533436;
BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                                                "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
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ACT_SITE 75 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 295890; CAB09331.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )1-FEB-1995 (Rel. 31, Created)
11-FEB-1995 (Rel. 31, Last sequence update)
5-DEC-1999 (Rel. 39, Last annotation update)
1-IDONATE REGULATORY PROTEIN.
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203 AA;
                                                                                                                                                                                                                  PEEKHAUS
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BY SIMILARITY.

BY SIMILARITY.

4 BY SIMILARITY.

2489 MW; 4D4FFD37 CRC32;
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                                  AND GNTT GENES
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!!AA_SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Plasmid ColN pCHAP4.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY
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PROSITE; PS00356; HTH_LACI_FAMILY; 1.

PFAM; PF00356; Hacī; 1.

PFAM; PF00532; Peripla_BP_like; 1.

Transcription regulation; DNA-binding; Gluconate utilization.
DNA_BIND

8
27
H-T-H MOTIF (POTENTIAL).

SEQUENCE 332 AA; 37567 MW; B4E1F229 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as rony modified and this statement is not remove entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                          "The immunity and lysis genes of ColN plasmid pCHAP4."; Mol. Gen. Genet. 211:335-341(1988).
                                                                                                                                                                                                                                                                              MEDLINE; 8817
PUGSLEY A.P.;
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Pr
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U14003; AAA97161.1; -
EMBL; AE000497; AAC77221.1;
HSSP; P03023; ILCD.
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REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
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TRANSMEM TRANSMEM SEQUENCE

124 15245 MW;

POTENTIAL POTENTIAL.

Transmembrane BA839D94 CRC32;

EMBL; X06933; CAA30020.1; -.
PIR; S01761; IMECN4.
Plasmid; Becteriocin; Colicin;
TRANSMEM 66 84 P(

IMMN_ECOLI

Length:

131

February

14,

2000 08:02

Type: P

Check: 6528

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II AA_SEQUENCE 1.0
ID IPRA_SAGSA
AC P31608;
DT 01-UUL-1993 (F
DT 01-UUL-1993 (F
DT 01-OCT 1993 (F
DE PROTEINASE INE
DE A) (API-A)
OS Sagittaria sag
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01-NOV-1990 (Rel. 1
01-NOV-1990 (Rel. 1
15-DEC-1998 (Rel. 3
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                         P31608:
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 27, Last annotation update)
PROTEINASE INHIBITOR A PRECURSOR (DOUBLE-HEADED
A) (API-A).
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"DNA sequence analysis of the imp UV protection and mu"

protection and mu"

prof the plasmid TPI10: identification of a third gene."

Nucleic Acids Res. 18:5045-5050(1990).

NUCLEIC ACIDS RES. 18:5045-5050(1990).
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PFAM; PF00817; IMS;
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Bacteria; Proteobacteria;
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Plasmid IncIl TP110.
        Sagittaria sagittifolia (Arrowhead).
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424 AA; 47786 MW; FE14F2F4 CRC32;
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Length: 181

February 14, 19152

2000

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151 101

VNGRTLLGIG

GEHFTVRFQK

FDALAMKTAP

KSTEETGVYK LAACSCEFCK IACPEVGSFN

YKFSFSMPVP LICDTAWSIG

51

AAIGFRGGLS

TLHKDACKSY

VYEAPETDRG

LPVGFSASAT DGDAVQLNLG 08:02

MAASNALLLI SGVLLISLAV LCHGDPVVDS

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SEQUENCE OF 25-174.

SEQUENCE OF 25-174.

SEQUENCE OF 25-174.

MEDITINE; 92316904.

"ANG H.-L., LUO R.-S., WANG L.-
"Primary structure and disulfid headed proteinase inhibitors.";

J. Biochem. 111:537-545(1992).

-i- FUNCTION: POSZESZEST TWO REF.

AMOUNT OF TRYPSIN AND CHYMO
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          ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida;
Alismataceae; Sagittaria.
                                                                                                                                                                                                                                                                              KALLIKREIN WEAKLY.
-!- SIMILARITY: STRONG, TO S.SAGITTIFOLIA PROTEINASE INHIBITORS B.
                                                                                                                                                                                                                                                                                                                                                                                                   VU W., TAO W., GONG Z., CHI C.-V
"CDNA and genomic structures of
J. Biochem. 113:153-158(1993).
                                                                                                                                       procease
            25
100
100
134
136
136
152
                                                                                                                                         inhibitor;
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SEQUENCE FROM N.A.
MEDLINE, 91155926.
RODICIO M.R., ALVAREZ M.A., CHATE
"Isolation and genetic structure
"Isolation for the inactivation
                                                                                                                                                                                                                                                _SEQUENCE 1.0
IS12 STRAL
                                                                                                                                                        IS12_STRAL STANDARD; PRT; 256 AA.

P23393;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
01-NOV-1991 (Rel. 20, Last annotation update)
INSERTION ELEMENT IS112 28.4 KD PROTEIN.
                                                                                                           Streptomyces albus g.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
             CHATER K.F.
scture of IS1
vation of the
             IS112, an the SalI
             restriction modification
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IS12_STRAL Length: 256
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         055274; P73884; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 36, Last annotation update) 15-JUL-1998 (Rel. 36, Last annotation update) IRON-STRESS INDUCED CHLOROPHYLL-BINDING PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.;
FERREIRA F., STRAUS N.A.;
Submitted (DEC-1993) to t
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Transposable element.
SEQUENCE 256 AA; 28409 MW; AD5CD17C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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MO1. Gen. Genet. 225:147-147(1991).
-!- FUNCTION: INACTIVATION OF SAL I RESTRICTION-MODIFICATION SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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Transmembrane.

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SOUTH THE REAL PROCESS OF THE PROCES
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                                                                                              PFAM;
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the Bacillus subtilis chromosome region between the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 141:205-2015(1996).

-! CATALYTIC ACTIVITY: 2-DEOXY-D-GLUCONATE + NAD(+) = 3-DEHYDRO-2-DEOXY-D-GLUCONATE + NADH.

-! DEOXY-D-GLUCONATE + NADH.
-! PATHWAY: PECTIN DEGRADATION.
-! SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
-FAMILY (SDR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
TRANSMEM
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ODMAIN
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                       HSSP; P19992; 2HSI
SUBTILIST; BG11400
PROSITE; PS00061;
                                                                                                                                                                                  EMBL; L47838; AAB38476.1; -.
EMBL; Z99115; CAB14131.1; -.
HSSP; P19992; 2HSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
MEDLINE; 96349105
SOROKIN A.V., AZEVEDO V.,
SERBOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #50842;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
7-DECXY-D-GLUCONATE 3-DEHYDROGENASE (EC 1.1.1.125) (2-KETO-3-
                                                   Oxidoreductase; NAD. NP_BIND 16
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Bacteria; Firmicutes;
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                                                                                         PF00106; adh_short; 1.
PF00678; adh_short_C2;
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254 AA;
                                                                                                                                                               BG11400; KDUD
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     WW;
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                     NAD (BY SIMILARITY)
BY SIMILARITY.
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EQAFDSLOT -> NKRL
; 889359C7 CRC32;
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S -> R (IN REF. 1).
EQAFDSLOT -> NKRLIPCK!
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451 PTAAELLEHP VFGAASG

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KDUD_BACSU Length:
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KR1_HSVBS

Q08097;

Q1-NOV-1995 ()

Q1-NOV-1995 ()
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BINDING
ACT_SITE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE (EC 27, 1.-).
BOVIDE herpesvirus type 1.2 (strain ST).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
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                                                                                                                                                                        101
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"The complete DNA sequence and the genetic organization of the short
unique region (US) of the bovine herpesvirus type 1 (ST strain).";
virology 199:409-421(1994).
                         351
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HSSP; P24941; 1AQ1.
401
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                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 94167875.
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                          RALFDSPAGP
                                                                                                                                            TREEAEGAAR
                                                                                                                                                                                                     EGSADLYLAV
                                                                                                                                                                                                                                  MERAAERLAR
                                                                                                                                                                                                                                                             Length: 467
                                                                                                                                                                                                                                                                                    s; Serine/threonine-protein kinase; ATP-binding.
164 462 PROTEIN KINASE;
170 178 ATP (BY SIMILARITY).
194 194 ATP (BY SIMILARITY).
194 194 194 BY SIMILARITY).
279 BY SIMILARITY.
467 AA; 49885 MW; 25EB1E22 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                              pkinase;
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                                                                                                                                             ALNFRIIRRL TPGSEGRVFE
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                         QGEDAEASGP
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                                                                                  KTENVFLNGP
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LSPA_MYCTU

202

February 14, 21345

2000

08:02

Type: P

Check:

2319

RRLRMLLSVA VVVLTLDIVT

MW;

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DOMAIN
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109 133 133 133

108 1108 1132 1132 1132

POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).

Hypothetical DOMAIN

PFAM;

Peptidase.

Hydrolase;

se; Aspartyl protease; Transmembrane CYTOPLASMIC (POTENTIAL).

PROSITE;

101

VVGIFWMGRR SVGWWPVFNV

> LVSPWWALGL GOPVSIIGDT PLTSTEEAGG

GMILGGAMGN

LVDRFFRAPG AAFSMATGYT

PLRGHVVDFL WVLTLIATGV

VTWTLVRNSG AGEPNAPAPP

KVVAVQLLPP MPDEPTGSAD Length:

151

ADPSVVGGAI LLVILSIFGF

201

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LSPA_MYC:
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MEDLINE: 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., COCLE S.T., BROSCH R., GAS S., BARRY C.E. III, TEKAIA F. GARDON S.V., EIGLMELER K., GAS S., BARRY C.E. III, TEKAIA F. BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R. DAVIES R., DEVLIN K., FEILWELL T., GENTLES S., HAMLIN N., HO DAVIES R., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J. RUTTER S., SEBGER K., SKELTON S., SQUARES S., SQARES R., SKILTON S., SULARES S., SQARES R., SKILTON S., BARRELL B.G.; THE BENOTIN THE BOOMER'S GROUND TO COMPLETE 99000ME SEQUENCE.";

NATURE 393:537-544(1998).
                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
PROBABLE LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36) (PROLIPOPROTEIN SIGNAL PEPTIDASE) (SPASE II)
SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II).
LSPA OR RV1539 OR MTCY48.26C.
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Bacteria; Firmicutes; Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210764;
                                                                                                                                                                                                                                           EMBL; Z74020; CAA98323.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      XAA IS HYDROPHOBIC (PREFERABLY LEU), XBB 15 OFTEN SEK ON SULFUR WITH A IS OFTEN GIV OR ALA, AND THE CYS IS ALKYLATED ON SULFUR WITH A DIACYLOLYCERYL GROUP.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY A8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL PEPTIDES FROM PROLIPOPROTEINS.
SIGNAL PEPTIDES FROM PROLIPOPROTEINS.
CATALYTIC ACTIVITY: CLEAVAGE OF N-TERMINAL LEADER SEQUENCES FROM MEMBRANE PROLIPOPROTEINS. HYDROLYSES XAA-XBB--|CYS, IN WHICH XAA IS HYDROPHOBIC (PREFERABLY LEU), XBB IS OFTEN SER OR ALA, XCC IS OFTEN GLY OR ALA, AND THE CYS IS ALKYLATED ON SULFUR WITH A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              utes; Actinobacteria; Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REAM M.A., ROGERS J.,
S., SQARES R., SULSTON
                                                                                                                                                                                                                                                                                                                                                     restrictions
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MAUF_PARDE
   SAFF
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                                                                                                                                                                                                                                                                             Transmembrane.
TRANSMEM 5.
TRANSMEM 5.
TRANSMEM 11
TRANSMEM 13
TRANSMEM 17
TRANSMEM 20
TRANSMEM 20
TRANSMEM 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHISTOSERDOV A.Y., BOYD J., MATHEWS F.S., LIDSTROM M.E.;
"A transcription-dependent DNase I-hypersensitive site in a far
upstream segment of the chicken alpha-globin gene domain coincides
with a matrix attachment region.";
Blochem. Blophys. Res. Commun. 184:1181-1189(1992).
-!- PATHMAY: METHYLAMINE UTILIZATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAN SPANNING R.J.M., DER PALEN C.J., SLOTBOOM D., REIJNDERS W.N., STOUTHAMER A.H., DUINE J.A.;
"Expression of the mau genes involved in methylamine metabolism in Paracoccus denitrificans is under control of a Lysk-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR.1993 (Rel. 25, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-NOY-1997 (Rel. 35, Last annotation updat
METHYLAMINE UTILIZATION PROTEIN MAUF.
                          MDH_RHILV
033525;
                                                    SEQUENCE
                                                                              251
                                                                                                        201
                                                                                                                                   151
                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U12464; AAA56723.1; -. EMBL; M90099; AAA25579.1; -. PIR; PH0856; PH0856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paracoccus denitrificans.
Bacteria; Proteobacteria;
 15-JUL-1998 (Rel. 15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 129-277 FROM N.A. MEDLINE; 92272712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcriptional activator.";
Eur. J. Biochem. 226:201-210(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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P29897;
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                                                                              RHQENAALAD
                                                                                                        LLYMMTLAAV
                                                                                                                                   AHQLDFLRVP
                                                                                                                                                                                       ASAAGPQPLW
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                                      STANDARD;
                                                                              GAILTALGAG
                                                                                                                                   YPORRAQVPH
                                                                                                                                                             YGLGALMLGG
                                                                                                                                                                                       AVLGAAAVAG
                                                                                                                                                                                                                SAGQASVPDC
 36,
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79
131
152
199
225
277
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                                                                                                                                                                                                                                                                    28361 MW;
Created)
Last sequence update)
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                                                                                                                                   DARQREPKWV
                                                                                                                                                             LLGGIGLIAG
                                                                                                                                                                                       GLLSTWSPCG YSSISLLRPD
                                                                                                                                                                                                                KLFPQSPSAA TRIAVLLAAA LAGAAGGVAL
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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7BE517A2 CRC32;
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                                                                                                                                 LDYLTYVQTP
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MDH_RHILV
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POOLE P.S., ALLAWAY D., SMITH M.;

POOLE P.S., ALLAWAY D., SMITH M.;

SUBMITTED (NOV-1997) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE +

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; FOURTH 1.

PROM; PEO0056; ldh; 1.

OXIDOTEQUECLASE; Tricarboxylic acid cycle; NAD.

OXIDOTEQUECLASE; Tricarboxylic acid cycle; NAD.

OXIDOTEQUECLASE; Tricarboxylic acid cycle; NAD.

PROTON-RELAY (BY SIMILARITY).

ACT_SITE 176 176 PROTON-RELAY (BY SIMILARITY).

ACT_SITE 200 AA: 33590 MW; 192E3E24 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     _SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            SEQUENCE FROM N.A.

STRAINERD / KW20;

MEDLINE; 95350630,

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M.,

MCKENLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

MCKENNEY K., SUTTON G., FITIZHUGH W., FIELDS C.A., GOCAYNE J.D.,

SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDDLOM E., COTTON M.D.,

UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,

FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                            P44689;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
PUTATIVE CELL CYCLE PROTEIN MESJ HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
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HSSP; Q27743; 1LDG.
PROSITE; PS00068; MDH; FALSE_NEG.
PFAM; PF00056; 1dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium leguminosarum ()
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, MALATE DEHYDROGENASE
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                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                MESJ OR
                                                                                                                                                                                                                                           laemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                            us influenzae.
Proteobacteria;
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a; alpha subdivision; Rhizobiaceae group:
                                                                                                                                                                                                                                                            gamma
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assembly of Haemophilus
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Whole-genome random sequencing and

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MESJ_HAEIN Length: 430
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P38371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32723; AAC22063.1; -.
                                                                            use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   Myxococcus xanthus.";
J. Bacteriol. 175:4756-4763(1993).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                       Myxococcales;
                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                           Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                        PUTATIVE LIPOPROTEIN MLPA PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenzae Rd.";
science 26:496-512(1995).
-i- SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science
                                                    EMBL; S64103; AAB27615.1; -. PIR; B40609; B40609.
                                                                                                                                                                                                                                                                      MARTINEZ-CANAMERO M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                        PROSITE;
                                                                                                                                                                                                                                           Oar, a 115-kilodalton membrane protein required for development of
                                                                                                                                                                                                                                                          NOUYE
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 0609; B40609.
; PS00013; PR
e; Signal; Li
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22 2
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(Rel. 30,
(Rel. 31,
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  ; Lipoprotein.
21 F
236 F
                                      PROKAR_LIPOPROTEIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
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POTENTIAL.
PUTATIVE LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                       Myxococcaceae;
                                                                                                              removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHYPKRPRED IKKIWQELGV
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e; Myxococcus.
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                                                                                                                              no on
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MML6_MYCTU

Length: 397

February 14, 2000 08:02

KRGWMVRSVF

DTIDGIDQLG

EQLASVIVIL

DKLAAIQPQL

101

AVKGTPMAGA GIYLAGTAAT

VGTVALSLGA

SEGLSVLVWQ

51

MQGISVTGLV VALLPDEIAS

QQINRELALA

NYATMSGIYA

QTAALIENAA AARMIISHEG

DPATPEGISH DLLIAGIAAL

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IIAA_SEQUENCE 1.0

IID MAIL_MYCTU
AC Q10773;
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SEQUENCE
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the SWISS Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodifies requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
PUTATIVE MEMBRANE PROTEIN MMPL6.
MMPL6 OR RV1557 OR MTCY48.08C.
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Bacteria; Firmicutes; Actin
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236 AA;
                                        al protein; Transmembrane.
161 181 POTENTIAL.
190 210 POTENTIAL.
214 234 POTENTIAL.
214 234 POTENTIAL.
242 262 POTENTIAL.
293 313 POTENTIAL.
293 313 POTENTIAL.
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GLVFAATMSS

FVFSDLRVLG

PRPASRMLRP

YGPRPVVREL LLREGNDDPR QIGTTIGLGL LEDTLVVRAF

TQVATHR MTPSIAVLLG AGTGGVVTAA

VLALAVILLL AVGSDYNLLL ISRFKEEIGA GLNTGIIRAM

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CHISTOSERDOVA L.V., LIDSTROM M.E.;
"Genetics of the serine cycle in Methylobacterium extorquens
identification of sgaA and mtdA and sequences of sgaA, hprA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
15-7UL-1999 (Rel. 38, Last annotation update)
METHYLENETETRAHYDROFOLATE DEHYDROGENASE [NAD+]
                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                              01-NOV-1995 (Rel. 32, C)
01-NOV-1995 (Rel. 32, L)
15-JUL-1999 (Rel. 38, L)
NEUROMEDIN B PRECURSOR.
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Oxidoreductase; NAD; One-carbon met
SEQUENCE 288 AA; 29736 MW; DEC1
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Bacteria; Proteobacteria; alpha
SEQUENCE FROM
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SIMILARITY: ONLY DISTANTLY RELATED TO THE OTHER 5,10-METHYLENE-THF
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Z.A.
                                                                                                                                                   STANDARD;
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32, Last sequence up
38, Last annotation
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                                        Amphibia;
Xenopodinae;
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PEPTIDE
MOD_RES
SEQUENCE
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PROSITE;
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MEDLINE; 93028554.
WECHSELBERGER C., KREIL G., RICHTER K.;
WISCHARTON and sequence of a cDNA encoding bombosin-like peptide from brain and early beautiful and control of the control of th
                                                                                                                                                                                                         Bombesin
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               MW;
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Cleavage on
           NEUROMEDIN B.
AMIDATION (G-55 PROVIDE AMIDE GROUP)
F9870792 CRC32;
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NEUB_XENLA Length: 120 February 14, 2000 08:02 Type: Ъ Check: 1414

Н MSAVPLTRML PLRFLTHLLL LSFIPLYFCM EFSEDARNIE KIRRGNQWAI

51 GHFMGKKSLQ DTYNPSEQDM DSEDFRPRII EMIRGTFRQE PIRALSPRKQ

DEIQWMLKKI MDDYIKTTQK

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!!AA_SEQUENCE 1.0
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                                                                                               ARNOLD W., RUMP A., KLIPP W., PRIEFER U.B., PUHLER A.; "Nucleotide sequence of a 24,206-base-pair DNA fragment entire nitrogen fixation gene cluster of Klebsiella pneu U. Mol. Biol. 203;715-738(1988).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 89041575.
BEYNON J., CANNON M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella pneumoniae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last seq
01-FEB-1994 (Rel. 28, Last ann
                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89094839.
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EMBL; X13303; CAA31670.1; -.
PIR; S01838; S01838.
Nitrogen fixation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIL F., CHANG P.-K., CARY J., LINZ J.E.;

"Structural and functional analysis of the nor-1 gene involved in the blosynthesis of aflatoxins by Abpergillus parasiticus.";

Appl. Environ. Microbiol. 60:4078-4085(1994).

-i- FUNCTION: MAY BE INVOLVED IN THE DEHYDRATION OF NORSOLORINIC ACII

-i- FORM AVERANTIN.

-i- PANHWAY: AFLATOXIN BIOSYNTHESIS.

-i- PANHWAY: AFLATOXIN BIOSYNTHESIS.

-i- SAMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

FAMILY (SDR). STRONG, TO E.NIDULANS STCE.
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15-DEC-1998 (Rel. 37, Last annotation update)
AFLATOXIN BIOSYNTHESIS KETOREDUCTASE NOR-1 (EC 1.1.1.-).
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                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus parasiticus.
Eukaryota; Fungi; Ascomycot
Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                  EMBL; L27801; AAA58798.1; PROSITE; PS00061; ADH_SHOI
                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95085270.
TRAIL F., CHANG P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=ATCC 163 /
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51
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                                                   MNGSLSQHDQ
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185
271 AA;
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208
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                                                                                                                                                                                                                                               adh_short;
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                                                   ERLSTPYRDG
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35, Last sequence 37, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ascomycota; Euascomycetes; Plectomycetes; ocomaceae; mitosporic Trichocomaceae; Aspe
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229
                                                                                                                                                                                                                                                                        ADH_SHORT; FALSE_NEG.
                                                                                                                                                 52
185
29569 MW;
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                                                                                                   February 14,
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     VAEGSRMIIV
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GLTGITLWKNAFFNPCFVLVAR
(IN REF. 2).
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                                                                                                                                                 A4798D11 CRC32;
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SIMILARITY.
                                                                                                   2000
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     QLNSDSETDA
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HGVTHLDVVV ANAAMATNFG PASTMPLEHL QAHMMVNMYA PVLLFQATRI

UBIQUINONE

NAD(+)

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CCC PART AND THE PART OF THE P
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                                                SEQUENCE FROM N.A.
MEDLINE; 94141942.
QUINN T.W., WILSON A.C.;
"Sequence evolution in a
"Sequence evolution in a
birds.";
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01-MAR-1992 (Rel. 21, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
MEDLINE; 91178819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.
MIND1 OR ND1 OR NADH1.
Coturnix coturnix japonica (Japanese quail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NU1M_COTJA
P24968;
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J. Mol. Evol. 32:153-16(1991).
j. CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
j. CATALYTIC ACTIVITY: NADH + UBIQUINONE I SUBUNIT 1 FAMILY.
j. SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
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                                                                                                                                                                                                                                                          031651;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
NADH-UBIQUIONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).
MINDS OR NADH5.
Anser caerulescens (Goose).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1.0
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PROSITE; PS00668; COMPLEX1_ND1_2; PARTIAL.
PEAM, PF00146; NaDHdh; 1
Oxidoreductase; NAD; Ubiquinone; Mitochond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X57246; CAA40522.1; -. PIR; S25422; S25422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                             Weognathae; Anseriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ب
      Mol. Evol. - CATALYTIC
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                                                                                                                                                                                                                                     Metazoa; Chordata;
      37:417-425(1993)
ACTIVITY: NADH +
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                                                                                                                                                                                                             ata; Craniata; Vertebrata;
Anatidae; Anser.
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                                                                                 the mitochondrial control
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Coturnix.
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ID NUHM_NEUCR
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its population by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      EMBL; L06178; AAB96808.1; -.
Oxidoreductase; NAD; Ubiquin
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-THORAX;
MEDLINE; 93114603.
CROZIER R.H., CROZIER Y.C.;
The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization.";
Genetics 133:97-117(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P34857;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1.0
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                                                   151
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                                                                                  101
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoidea; Apidae; Apis.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apis mellifera ligustica (Common honeybee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSVDLQPSLN TSYLNTWALL LTLMATAFTA TYSIRMTILV QAGQTRIPPM
                                                   LMTKITYIEK KTLRKKK
                                                                                  IIITMKIYNK LSQNEHYFNY
                                                                                                                                                        MMLTIIMLSK IFMSSLISMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 AA;
                                                                                                                                                                                                                           ΑΑ,
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                                                                                                                      ILMILIVFLS
                                                                                                                                                                                       February 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23230 MW;
                                                                                                                                                                                                                         ; Ubiquinone; Mitochondrion.
19971 MW; 36B64E1B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGPEGLAELQ VAASKAATSM HTGLIKAYLG
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                                                                                    FKNIDLMYLY
                                                                                                                      GMLIMFSYFI
                                                                                                                                                        LTIYLNNIFN
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                                                                                    MKMNSTLFFI MILMLIITLE
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                                                                                                                                                                                       08:02 Type: P
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                                                                                                                                                        SYSIYMSLMM
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STANDARD;

PRT;

263

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BERRRE

NUKM_BRAOL STANDARD; PRT; 215 AA. P42027; 210. NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) NADH-UBIOUTIONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD).

!!AA_SEQUENCE 1.0

SEPYGPEVTR

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W SEQUENCE FROM N.A.

X MEDLINE; 95034970.

X MEDLINE; 95034970.

RA AZEVEDO J.E., DUARTE M., BELO J.A., WERNER S., VIDEIRA A.;

RA COMPLEMENTARY DNA SEQUENCES OF the 24 kDa and 21 kDa subunits of RI COMPLEX I from Neurospora.";

RI COMPLEMENTARY DNA SEQUENCES OF the 24 kDa and 21 kDa subunits of RI COMPLEX I from Neurospora.";

RI BIOCHIM. BiOPHYS. Acta 1188:159-161(1994).

CC -!- FUNCTION: TRANSFER OF ELECTRON SERON WADH TO THE RESPIRATORY COMPLEX I SELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)

CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.

CC -!- SUBUNIT: COMPONENT OF THE FLAVOPROTEIN FRACTION.

CC -!- SUBUNIT: SIS A COMPONENT OF THE FLAVOPROTEIN FRACTION.

CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 24 KD SUBUNIT FAMILY.

CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 14 KD SUBUNIT FAMILY.

CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 14 KD SUBUNIT FAMILY.
                                                                                                                                                                                                                                   NUHM_NEUCR Length: 263 February 14, 2000 08:02
                                                                                                                                                                                                                                 METAL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P40915;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBLOUIONE OXIDOREDUCTASE 24 KD SUBUNIT (EC 1.6.99.3).
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Eukaryota; Fungi; Ascomycota; Euascomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X78083; CAA54990.1; -
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                                                                                                                                                         4
                                                                                                                                                         MATKLTPFLM RTAVRAATRL
  DYFEDLTPET
                                                                              CSISVMNEVA
                                                                                                                     NTPDNNPDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                   re; ps01099; COMPLEX1_24K; 1.
pr01257; complex1_24kD; 1.
                                                                                                                                                                                                                                      263 AA;
                                                                                                                                                                                                                                                        143
148
186
190
IKQVLSALKE
                                                                              RLLEMPPMRV
                                                                                                                FKFSADNEKV
                                        AIKEHLGIKQ
                                                                                                                                                                                                                                                          143
148
186
190
                                                                                                                                                                                                                                                                                                                                                    42
263
                                                                                                                                                                                                                                      28842 MW;
  SVTDVSKAPQ PGPQSGRQTC ENAAGLTSLT
                                          GETTPDGLFT
                                                                              YEVASFYTMY
                                                                                                                   IEEIIKRYPP
                                                                                                                                                         STKPSTIAPV SRACLSISAR RPSDTLMVHR
                                                                                                                                                                                                                                   MITOCHONDRION (POTENTIAL).

NADH-UBIQUINONE OXIDOREDUCTASE 24 KI
SUBUNIT.

IRON-SULEUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).

IRON-SULFUR (2FE-2S) (POTENTIAL).
                                          FIEVECLGAC
                                                                              NRTPVGKFHV
                                                                                                                   QYKKAAVMPL
                                                                                                                                                                                             Type: P Check: 3961
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
SEQUENCE FROM N.A.
STRAIN-K12 / ANS87;
MEDLINE; 9389724.
MEDLINE; 9389724.
The gene locus of the proton-translocating NADH: ubiquinone "The gene locus of the proton-translocating NADH: ubiquinone oxidoreductase in Escherichia coli. Organization of the 14 genes relationship between the derived proteins and subunits of
                                                                                                                                                                                                                                                                                                                                                                                             P33605; P78236; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 35, Last sequence up 01-NOV-1997 (Rel. 35, Last annotation NADH DEHYDROGENASE I CHAIN J (EC 1.6.: OXIDOREDUCTASE CHAIN 10) (NUO10).
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Oxidoreductase; NAD; Ubiquinone; Mitochondrion;
Iron-sulfur; 4Fe-45.
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TRANSIT
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215
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NADH-UBIQUINONE OXIDOREDUCTASE 20 KD
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                                                                                                                                                                                                                                                                                                           subdivision;
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1.6.5.3) (NA
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                                                                                                                                                                                                                                                                                                           Enterobacteriaceae;
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ID NUZM_NEUCR
AC P19968;
DT 01-FEB-1991 (

STANDARD;

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ILGVNDQGID EERAGEVLSN

GTPISAKAVG RKDDSAKRKT

AIMLVVIVYA GLVVAFHVGR AGALEIIVYA

GAIMVLFVFV VMMLNLGGSE

IEQERQWLKP ITLFGPYVLA

QVWIGPAILS

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NUOJ_ECOLI Length: 184
                                                                                                                    PFAM; PEO0499; OJ
OXIGOTGOUCTAGE;
ITRANSMEM 1
ITRANSMEM 28
ITRANSMEM 54
ITRANSMEM 92
ITRANSMEM 92
ITRANSMEM 138
CONFLICT 85
CONFLICT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIBAH, BABAT, FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KINA S., KIUNGA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
KASHIMOTO K., KIK S., KIUNGA S., KITAGAWA M., KITAKAWA M., MAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., MISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
SADMITHE (JAN-1997) to the EMBL/GenBank/DDBJ databases

1 FUNCTION: TARANSFER OF ELECTRON FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON SFROM NADH TO THE ENZYME IS BELLEVED
TO BE UBIQUILMONE. DOSES COUPLE THE REBOX REACTION TO PROTON
TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON

TRANSLOCATION AND THUS CONSERVES THE REDOX ENERGY IN A PROTON
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SIRAIN-K12 / MG165;
MEDLINE: 97426617.
MEDLINE: 97426617.
MEDLINE: 97426617.
MEDLINE: 97426617.
MEDLINE: 97426617.
MAYIEW G. III, BLOCH C.A., PERNA N.T., BURLAND BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYIEW G.F.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYIEW G.F.
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitochondrial J. Mol. Biol.
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9L; D90859; CAB22037.1; -.
87; S37067; S37067.
87; S38319; S38319.
938319; S38319.
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CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS NUOA, H, J,

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE SECTOR OF THE COMPLEX.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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  MEFAFYICGL
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233:109-122(1993).
  IAILATLRVI
                                              February 14, 2000
                                                                                              19874 MW;
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A -> R 29FD5B12
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P31132; P76026; P77550;

O1-7U1-1993 (Rel. 26, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

O1-NOV-1997 (Rel. 35, Last annotation update)

O1-NOV-1997 (Rel. 35, SYSTEM PERMEASE PROT
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97 / AG1655;
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PODE C.K., MAYHEW G.F.,
GREGGR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE; 90147712.

VIDEIRA A., TROPSCHUG M., WERNER S.;

VIDEIRA A., TROPSCHUG M., VITO expression and import into mitochondria primary structure, in vitro expression and import into mitochondria of a 29/21-kDa subunit of complex I from Neurospora crassa.";

Blochem. Biophys. Res. Commun. 166:280-285(1990).

IF FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.

TO BE UBIQUINONE.

IF SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.

SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE. IMPORTATION INTO MITOCHONDRION IS MEMBRANE POTENTIAL DEPENDENT.
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       AIBA H., BAI
                                                                  SEQUENCE FROM N.A.
STRAIN-K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                 Science
                                                                                                                                                                                             "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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Eukaryota; Fung1; Ascomycota; Euascomycetes;
Sordariales; Sordariaceae; Neurospora.
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15-DEC-1998 (Rel. 37, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 21.3 KD SUBUNIT (EC 1.6.5.3)
(EC 1.6.99.3).
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                                                                                                                                                          complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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                                          BABA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteobacteria;
          INADA
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   FUJITA K., HAYASHI K., HONJO
T., ISONO K., ISONO S., ITOH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Enterobacteriaceae;
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HORIUCHI T.,
KANAI K., KASAI
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AC P08005;
DT 01-AUG-1988 (F

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GAAAFFLAVI AKYHĻNDPIM

LGVSAGVIAA TOYFSYLKOL

LKQNTKWDYT AHGDFGPSFK

VMGLAMTGVV IPSFVVAPLI

YKDYSVNDLV ASSFPVSAKI

LPGGGWNGGA

LKEMILPMVA

LSLAYIASIA

51

MLKFILRRCL EAIPTLFILI

TISFFMMRLA PGSPFTGERT LPPEVMANIE

201

LHSNFIRTAR VMIFAIILHW

AKGLPMRRII QLFVNGALNR

LRHALKPALL PVLSYMGPAF VGIITGSMVI

ETIYGLPGIG

DYSLVLSLTI

LVGALTILEN AIVDVLYAVI

P08005; 01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last seg

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PRAM; PF(
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YIGANTINA, "THE TOTAL TO THE POLYMINE-INDUCED PROTEIN AS A PETIPLASMIC OLIGOPEPTICAL PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.

-!- SUBSTRATE ACROSS THE MEMBRANE PROTEIN. INNER MEMBRANE.
-!- SUBSTLULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-!- SUBSTLULIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000223; AAC74326.1; --
EMBL; D90763; CAB20709.1; --
EMBL; D90552; CAB21967.1; --
EMBL; J05433; --
EM
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TE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
PF00528; BPD_transp; 1.
      Length: 306
                                                   528; BPD_transp; 1.
Peptide transport;
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30
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121
137
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271
February 14, 2000 08:02 Type: P Check:
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                                                         MW.
                                                   CYTOPLASMIC (PROBABLE)
3FCCC9F5 CRC32;
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EXTRACELLULAR (PROBABLE)
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CYTOPLASMIC (PROBABLE).
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EXTRACELLULAR (PROBABLE)
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DOMAIN
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Mol. Microbiol. 6:47-57(1992).
-i- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT
FOR OLIGOPEPTIDES; PROBABLY RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, 1
OLIGOPEPTIDE TRANSPORT
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"Molecular characterization
Salmonella typhimurium.";
J. Mol. Biol. 195:125-142(19
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PIR; B29333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a capen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
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PS00402; BPD_TRANSP_INN_MEMBR; 1.
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Proteobacteria;
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T SYSTEM PERMEASE PROTEIN OPPB
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S OF OTHER BINDING-
TO THE OPPER
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01-AUG-1991 (Rel.
01-AUG-1991 (Rel.
01-DEC-1992 (Rel.
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MEDILINE; 91009258.

HUBER A., SMITH D.P., ZUKER C.S., PAULSEN R.;

HUBER A., SMITH D.P., ZUKER C.S., PAULSEN R.;

"Opsin of Calliphora peripheral photoreceptors R1-6. Homology with

"Opsin of Calliphora peripheral processing.";

J. Biol. Chem. 265:17906-17910(1990).

-i- FUNCTION: VISUAL PICKENTS ARE THE LIGHT-ABSORBING MOLECULES THA

MEDIATE VISION. THEY CONSIST OF AN APPOPROTEIN, OPSIN, COVALENTI

LINKED TO CIS-RETINAL.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- FIM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES M

BE PHOSPHORYLATED.

-I- MISCELLANEOUS: EACH EYE IS COMPOSED OF 800 FACETS OR OMMATIDIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U1-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
OPSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as lon-
modified and this statement is not remov-
entities requires a license agreement (So-
or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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GCRDB; GCR_0009
                                                                                                                                                                                                                                                                                     GLYCOPTOTEIN;
                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1. PROSITE; PS00238; OPSIN; 1.
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                                                                                                                                                                           CRANSMEM
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                                                                                                                                                                                                                                                                                                                      Photoreceptor;
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EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
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7 (POT)
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CYTOPLASMIC.
RETINAL CHROMOPHORE 6D98882F CRC32;
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CYTOPLASMIC.
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EXTRACELLULAR
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CYTOPLASMIC.
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                                                                                               (POTENTIAL)
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AL SER OR THR RESIDUES MAY
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OPS1_CALVI Length:

371

February

14,

2000

08:02

Type:

Check:

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MERYSTPLIG

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PAMEPKWAKE ש

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EMBL; K02315; AAA28733.1; AI
EMBL; K02320; AAA28735.1; AI
EMBL; K02316; AAA28735.1; JU
EMBL; K02317; AAA28735.1; JU
EMBL; K02318; AAA28735.1; JU
EMBL; K02318; AAA28735.1; JU
EMBL; K02319; QAA28735.1; JU
EMBL; K02319; QAA28735.1; JU
EMBL; GCR_0028;
GCRDB; GCR_0029;
                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
ZUKER C.
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OPS1_DROM
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Eukaryota; Metazoa; Arthropoda; Tacheata; Hexapoda; Insecta;
Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUKER C.S., COMMAN A.F., RUBIN G.M.;
"ISOLATION and structure of a rhodopsin gene from D. melanogaster.";
Cell 40:851-858(1985),
-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
MEDIARE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
LINKED TO CIS-RETINAL.
INTEGRAL MEMBRANE PROTEIN.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 85176937.
O'TOUSA J.E., BAEHR W.,
APPLEBURY M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 85176937.
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13-AUG-1987 (Rel. 05, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
OPSIN RH1 (OWTER R1-R6 PHOTORECEPTOR CELLS OPSIN).
RH1 OR NINAE.
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MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR OMMATIDIA. EACH OMMATIDIUM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8), THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER CELLS.

CELLS.

MISCELLANEOUS: OPSIN RH1 HAS AN ABSORPTION MAXIMA AT 480 NM.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

OPSIN SUBFAMILY.
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FBgn0002940; ninae.
PS00237; G_PROTEIN_RECEPTOR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAK W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCPCCVFGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIINTLGLFK
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                                                                                                                                                                                                                                                                  collaboration
                                                                                                                                                                                                   .ch/announce/
                                                                                                                                                                                                                                    n 0
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IIAA_SEQUENCE 1.0
ID OPS1_DROPS
AC P28678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPS1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-APPLE HILL;

MEDLINE; 93012921.

CARULLI J.P., HARTL D.L.;

CARULLI J.P., HARTL D.L.;

CYARIABLE rates of evolution among Drosophila opsin genes.";

Genetics 132:193-204(1992).

-!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
DISULFID
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
DOMAIN
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DOMAIN
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DOMAIN
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                        Drosophila pseudoobscura (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Ptarygota: Neoptera: Endopterygota: Diptera; Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1995 (Rel. 32, Last sequence update)
01-REB-1996 (Rel. 33, Last annotation update)
OPSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN).
                                                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                             RH1 OR NINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photoreceptor; Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00238; OPSIN; PFAM; PF00001; 7tm_1; 1.
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LINKED TO CIS-RETINAL.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
BE PHOSPHORYLATED.

BE PHOSPHORYLATED.

MISCELLANEOUS: EACH DROSOPHILA EYE IS COMPOSED OF 800 FACETS OR
OMAGATIDIA. EACH OWMATIDIM CONTAINS 8 PHOTORECEPTOR CELLS (R1-R8)

THE R1 TO R6 CELLS ARE OUTER CELLS, WHILE R7 AND R8 ARE INNER
CELLS.

MISCELLANEOUS: OPSIN RH1 HAS AN ABSORPTION MAXIMA AT 480 NM.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                          KVDDGKSSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                   FKFEGLTPLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAKKMNVKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIVKGMAGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILTAYMIMI GMISWCGNGV VIYIFATTKS LRTPANLLVI NLAISDFGIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITNTPMMGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESFAVAAAQ LGPHFAPLSN GSVVDKVTPD MAHLISPYWN QFPAMDPIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 373
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86

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113

126

147

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200

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                                                                                                                                                                                                                                                                                                                                                                                                         OSQATASEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                  TIWGACFAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSSEDAEKSA EGKLAKVALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTIPLALGKI AYIWFMSSIW CLAPAFGWSR YVPEGNLTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYFETWVLGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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EXTRACELLULAR.
5 (POTENTIAL)
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EXTRACELLULAR.
3 (POTENTIAL)
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CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
CYTOPLASMIC.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
RETINAL CHROMOPHORE.
; 43B10BFA CRC32;
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CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                    374
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                                                 OR
1-R8),
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OPSIN SUBFAMILY

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RRA RRA
                                                                                                                                                                                                                                                                                                                                                     OPS1_DROPS
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DISULFID
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                          OTCA_VIBS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X65877; CAA46708.1; -.
PIR; S24605, S24605.
GCRDB; GCR_0429; -.
GCRDB; GCR_0509; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as 100 as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLYBASE; FBgn0012733; Dpse\ninaE.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
PROSITE; PS00238; OPSIN; 1.
PFAM; PF00001; 7tm_1; 1.
          SEQUENCE FROM N.A.
LIANG Z.Y., DEMARE
GLANSDORFF N.;
                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ORNITHINE CARBAMOYLTRANSFERASE, ANABOLIC (EC
                                                                                                                                                                           351
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Submitted (FEB-1997) to
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                                                    Vibrio sp. (strain 2693).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                           GKYDDGKSSE AQSQATTSEA
                                                                                                                                                                                              LFKFEGLTPL NTIWGACFAK SAACYNPIVY
                                                                                                                                                                                                                                           CGIDYLERDW
                                                                                                                                                                                                                                                                                                           KILTAYMIII GMISWCGNGV VIYIFATTKS LRTPANLLVI
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                                                                                                                                                                                                                                                                                                                                                       Length:
                    DEMAREZ M.,
                                                                                                                                                                                                                                                                                                                                                       374
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                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                       LRSSEDADKS
                                                                                                                                                                                                                                                                 MTIPLALGKI
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the
                     LEGRAIN C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coup
                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                    gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                           ESKA
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                                                                                                                                                                                                                       AEGKLAKVAL
                                                                                                                                                                                                                                                                                                                                                                                                                     6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
CYTOPLASMIC.
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
RETINAL CHROMOPHORE.
AACD8CB5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE
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EXTRACELLULAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed receptor;
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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                     BAETENS M., ROOVERS
                                                                                                                                          301
                                                                                                                                                                                                                                                                                     SAFGCSSIWS
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                                                                                     2.1.3.3)
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                                                                                     (OTCASE).
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OTCA_VIBS2 Length: 301
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OTC_SCHPO
P31317;
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                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
ORNITHINE CARBAMOYLIRANSFERASE PRECURSOR (E
(ORNITHINE TRANSCARBAMYLASE).
ARG3 OR SPAC469.10.
                                                                                                                                                                                                  VAN HUFFEL C., DUBOIS E., MESSENGUY F.;
"Cloning and sequencing of arg3 and arg11 genes of
Schizosaccharomyces pombe on a 10-kb DNA fragment. Heterologous
expression and mitochondrial targeting of their translation
products.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
-!- SUBCULULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiasomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P04391; 1AKM.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
PFAM; PF00185; OTCace; 1.
Arginine biosynthesis; Transferase.
SEQUENCE 301 AA; 32825 MW; 3CA3E90D CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y11033; CAA71921.1; -. HSSP; P04391; 1AKM.
                      -I- PATHWAY: FIRST STEP IN ARGININE BIOSYNTHESIS.
-I- SUBCELLULAR LOCATION: MITOCHONDRIAL MARRIX.
-I- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                      MEDLINE; 92
VAN HUFFEL
                                                                                                                                                                                                                                                                                     STRAIN-975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: CARBAMOYL PHOSPHATE + ORNITHINE - CITRULLINE
                                                                                                                                   STRAIN-972;
                                                                                                                                                                                              products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 chizosaccharomyces.
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                                                                          ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORTHOPHOSPHATE
                                                                                                                                                                               Biochem.
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 entry
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                                                                                                                                                                               205:33-43(1992).
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copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRECURSOR (EC
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   is
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 produced through
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                                                                                                                      WALSH S.V.;
                                                                                          CITRULLINE
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   collaboration
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SON THE WAR AND THE COLOR COLO
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUS-KIDNEY CORTEX;
TISSUS-KIDNEY CORTEX;
MEDLINE; 97220379.
SIMONIC T., DUGA S., NEGRI A., TEDESCHI G., MALCOVATI M.,
TENCHINI M.L., RONCHI S.;
TENCHINI M.L., RONCHI S.;
TENCHINI M.I., RONCHI S.;
TENCHINI M.I., RONCHI S.;
TEDNA CIONING and expression of the flavoprotein D-aspartate from bovine kidney cortex.";
Biochem. J. 322:729-735(1997).
-1- CATALYTIC ACTIVITY: D-ASPARTATE + H(2)0 + O(2) = OXALOACE
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beef
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
D-ASPARTATE OXIDASE (EC 1.4.3.1) (DASOX) (DDO).
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92291057.
NEGRI A., CECILIANI F.,
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PFAM; PF00185; OTCace; 1.
Arginine biosynthesis; Transferase; Mitochondrion; Transit peptide.
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EMBL; Z69727; CAA93560.1; -.
PIR; S2390; OWZP.
HSSP; Q51742; 1A1S.
                                                                                                                 NH(3) + H(2)O(2).
-!- COFACTOR: FAD OR 6-HYDROXYFLAVIN ADENINE
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: PEROXISOMAL.
-!- SIMILARITY: BELONGS TO THE DAMOX/DASOX FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-338.
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O THE DAMOX/DASOX FAMILY:
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ORNITHINE CARBAMOYLTRANSFERASE.
; 9CC43E5C CRC32;
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XX MEDLINE; 97306065.

XX MEDLINE; 98303(1997).

XY BLOCHEM, 121:798-803(1997).

XY MEDLINE; 9800(1997).

XY MEDLINE; 970065.

XY MEDLINE;
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01-NOV-1997
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D-ASPARTATE
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00342; MICROBODIES_CTER; 1.
PFAM; PF01266; DAO; 1.
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(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
OXIDASE (EC 1.4.3.1) (DASOX) (DDO)
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BY SIMILARITY.

MICROBODY TARGETING SIGNAL (
V -> I (IN SOME MOLECULES).
K -> R (IN REF. 1).
S -> G (IN REF. 1).
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ght. It is produced through a collaboration Bioinformatics and the EMBL outstation. Bittitte. There are no restrictions on its ns as long as its content is in no way not removed. Usage by and for commercial eement (See http://www.isb-sib.ch/announce/
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HSSP; P00371
MIM; 124450;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 97432828.
SOMERS G.R., HAMMET F., WOOI
VENTER D.J.;
"Chromosomal localization of
phylogenetic analysis of the
Genomics 44:127-130(1997).
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SEQUENCE
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Oxidoreductase;
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MEDILINE; 97415792.
MALIER R., GLATZ A., MOSBACHER J., BILBE G.;
MALIER R. GLATZ A., MOSBACHER J., BILBE G.;
"Cloning of P2Y6 CDNAs and identification of a pseudogene: cof P2Y receptor subtype expression in bone and brain tissues of P2Y receptor subtype expression in bone and brain tissues Biochem. Biophys. Res. Commun. 237:297-302(1997).
                                                                                                                                                                                                                                                                                                                                Genomics
[3]
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01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence up

15-DEC-1998 (Rel. 37, Last annotation

P2Y PURINOCEPTOR 6 (P276).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
    MEDLINE; 98069816.

MAIER R., GLATZ A., MOSBACHER J., BILBE G.;

BIOCHEM. BIOPHYS. Res. COMMUN. 240:298-302(1997).

PICTION: RECEPTOR FOR EXTRACELLULAR UDP > UTP > ATP.

OF THIS RECEPTOR IS MEDIAGED BY G PROTEINS WHICH ACTI

OF THIS RECEPTOR IS MEDIAGED BY GENOME SESSINGER SYSTEM.

PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED

-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FAD (ADP PART) (PO)
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                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00237; G_PROTEIN_RECEPTOR; PFAM; PF000001; 7tm_1: 1
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AF007891; AAB80712.1;
P34996; 1DDD.
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                            February 14, 2000 08:02
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                                                           MW;
RENFKQLLLP
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EXTRACELLULAR
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CYTOPLASMIC (FOTENTIAL)
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POTENTIAL.
MISSING (IN REF
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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                             Type: P
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MEDLINE; 92356828.

TOKITO M.K., DALDAL F.;

Tokito M.K., DALDAL F.;

"petR, located upstream of the fbcFBC operon encoding the cytochrome bcl complex, is homologous to bacterial response regulators and necessary for photosynthetic and respiratory growth of Rhodobacter capsulatus.";
                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel.
01-JUL-1993 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                    SEQUENCE FROM N.A. STRAIN-MT1131;
                                                                                                                                                                                                                            er capsulatus (Rhodopseudomonas capsulata).
Proteobacteria; alpha subdivision; Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Last sequence update)
Last annotation update)
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AKWQRQGF VPCTVLEAFA RQDGPAEPVA QRNRTVCYDL SFORYLGICH ADLLYACSLP

QERRGKAARM SPPALATHYM PLAPWHKRGG LLIYNYAQGD

AVVVAAAFAI

PYGMALTVIG

RRAAWLVCVA HWPFGDFACE

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I!AA_SEQUENCE 1.0

ID PEX3_YEAST
AC PAR995;
DT 01-DEC-1992 (ID 01-DEC-1992 (ID 01-NOV-1997 (ID
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                                                                                                                                                                                                                                                   p28795;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PAS3 (PEROXIN-3).
PEX3 OR PAS3 OR PD7392 OR D9798.15
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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MEDLINE; 91373453.
HOEHFELD J., VEENHUIS M., KUNAU W.-H.;
"PASJ, a Saccharomyces cerevisiae gene encoding a peroxisomal integral membrane protein essential for peroxisome biogenesis.";
J. Cell Biol. 114:1167-1178(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, Z12113; CAA78097.1; -.
PIR: S22631; S22631
PROSITE; PS01117; HTH_MARR_FAMILY; 1.
PFAM; PF01047; Marr; 1.
Transcription regulation; DNA-binding.
SEQUENCE 166 AA; 18807 MW; 99E3E86E CRC32;
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DOMAIN
SEQUENCE
EMBL; J04987; AAA21973.1; -.
PIR; B34340; RDALAE.
HSSP; P19992; 2HSD.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_Short; 1.
PFAM; PF00678; adh_Short_C2; 1.
Oxidoreductase; NADP; PHB biosynthesis.
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-116;
MEDLINE; 89359356.
MEDLINE; 89359356.
MEDLINE; 89359356.
PALPLES O.P., SINSKEY A.J.;
PEOPLES O.P., SINSKEY A.J.;
Characterization of the genes encoding beta-ketothiolase cacetoacetyi-CoA reductase.";
J. Biol. Chem. 264:15293-15297(1989).
-1- CATALYTIC ACTIVITY: (R)-3-HYDROXYACYI-COA + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P14697;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
ACETOACETYL-COA REDUCTASE (EC 1.1.1.36).
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EMBL; U32517; AAB64764.1;
PIR; A40550; A40550.
SGD; L0001339; PAS3.
Transmembrane; Peroxisome.
                                                                                                                                                                                                                              -i- PATHWAY: SECOND STEP IN POLY-BETA-HYDROXYBUTYRATE BIOSYNTHESIS.
-i- SUBCELIDLAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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COA + NADPH.
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441 AA;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL);
9C648B96 CRC32;
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PHBB_ALCEU Length: 246 February 14, 2000 08:02 Type: P
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ACT_SITE
SEQUENCE
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CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

CHEN C.-M., YE Q.-Z., ZHU Z., WANNER B.L., WALSH C.T.;

sequencing of the phn (psib) genes involved in alkylphosphonate sequencing of the phn (psib) genes involved in alkylphosphonate uptake and C.-P lyase activity in Escherichia coli B.";

J. BIOL. Chem. 265:4461-4471(1990).

J. BIOL. Chem. 265:4461-4471(1990).

FOR ALKYLPHOSPHONATES; PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE TRANSPORT SYSTEM.
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                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat)
PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN
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STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 91193228.

MARKINO K., KIM S.K., SHINAGAWA H., AMEMURA M., NAKATA A.;

"Molecular analysis of the cryptic and functional phn operons phosphonate use in Escherichia coli K-12.";

J. Bacteriol. 173:2665-2672(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
EMMBL; D90227; BAA14271.1; -.
EMMBL; U14003; AAA96996.1; -.
EMMBL; AE0000482; AAC77058.1;
EMMBL; A50506; AAA24349.1; -.
PIR; C35719; C35719.
ECOGENE; EG10720; PHNK.
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[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the region from 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95334362.
BURLAND V.D., PLUNKETT
BLATTNER F.R.;
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246
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                                                                                                                                                            restrictions
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II AA_SEQUENCE 1.0
II D FIRA_ORYSA
AC Q40708;
AC Q40708
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PI7A_ORYSA
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PFAM; PF00005; ABC_Tran; 1.

PFAM; PF00005; ABC_tran; 1.

RETAIN 45 ATP (BY SIMILARIY)

SEQUENCE 47 47 L -> 0 (IN REF. 2)

SEQUENCE 252 AA; 27831 MW; CBE59E63 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR7A PROTEIN.

Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;

Poaceae; Oryza.
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                                                                                                                                                                     EMBL; Z34271; CAA84025.1; -. HSSP; P52704; 1YAS. PFAM; PF00561; abhydrolase;
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01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
                                                                                                                                                 Hydrolase; Serine esterase.
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Length: 263
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263 AA;
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February 14, 2000 08:02 Type: P
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AAAGAHPARA

LYNRSPPEDL TLATMLVRPG

HSLGGLSLAL FFMDSKTIVL TNYIDDPIMK

AMERFPDKVA NTNQEPRTAV DETLLTEGNY

QRWTIDLSPG VEVEELAGAD

HMAMCSKPRE

RPLLDAVAAA AAGKHMGITL

APGERLVLVG EEFMRRIKPD

!!AA_SEQUENCE

SYNY3 LCDLLLRIAA

STANDARD;

PRT;

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Last sequence up Created)

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DOMAIN
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SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                  PDB; 1PCS; 17-DEC-97.

PROSITE; PS00196; COPPER_BLUE; 1.

PFAM; PF00127; Copper-bind; 1.
                                                                                                                                                                                                                                                                             EMBL; X54105; CAA38038.1; -.
EMBL; D64000; BAA10227.1; -.
PIR; S13733; S13733
PDB; 1PCS; 17-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The 2.15 A crystal structure of a triple mutant plastocyanin from the cyanobacterium synechocystis sp. PCC 6803.";
J. Mol. Biol. 275:327-335(1998).

"IF FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P700 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I.

"IT INDUCTION: BY COPPER."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 96127529.

TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,

KANEKO T., TANAKA A., SATO S.,

SUGIURA M., TABATA S.;

"Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb

region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 91338701.

MEDLINE; 91338701.

MEDLINE; 91338701.

"Copper-induced expression, cloning, and regulatory studies

"Copper-induced expression, and a copper-induced expression, and a copper-in
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DE LA ROSA M.A.;
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MEDLINE; 97443974.
SAZUKA T., OHARA O.;
"Towards a proteome project of cyanobacterium Synechocystis sp.
strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- INDUCTION: BY COPPER.
-1- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
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Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 9812879
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                       ; Copper;
28
126
126
17
111
111
111
111
  Œ,
                                                                                                                                                                                     Signal; 3D-structure
                                                                         COPPER.
                                                                                                                    PLASTOCYANIN.
PLASTOCYANIN-LIKE
0358BFF1 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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PCC
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PLAS_SYNY3
                                         CA_BIND
DOMAIN
DOMAIN
   SEQUENCE
                                                                                                                                                                                 EMBL; X07743; CAA30564.1; -.
PIR; S00755; S00755
PIR; A45762; A45762
PDB; 1PLS; 03-JUN-95.
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                "Solution structure of a pleckstrin-homology domain.";
Nature 369:672-675(1994).
-i- FUNCTION: MAJOR PROTEIN KINASE C SUBSTRATE OF PLATELETS,
EXACT FUNCTION IS NOT KNOWN.
-i- SIMILARITY: CONTAINS 2 PH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _SEQUENCE 1.0
PLEK_HUMAN
                                                                                              PROSITE; PS50003; PH_DOMAIN;
PFAM; PF00169; PH; 2
PFAM; PF00610; DEP; 1.
PFAM; PF00610; DEP; 1.
Phosphorylation; Repeat; 3D-s
DOMAIN 107 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 89359547.
TYERS M., HASLAM R.J., RACHUBINSKI
"Molecular analysis of pleckstrin:
"Molecular analysis of pleckstrin:
substrate of platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYERS M., RACHUBINSKI R.A., MCCAW M.L., VARRICHIO A.M., SHORR R.G.L., HASLAM R.J., HARLEY C.B.; "Molecular cloning and expression of the major protein kinase substrate of platelets."; nature 333:470-473(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94268557.
YOON H.S., HAJDUK P.J.,
FESIK S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 1-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Cell. Biochem. 40:133-145(1989)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation updat
PLECKSTRIN_(PLATELET P47 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
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350 AA;
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 40082 MW;
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                                                                                3D-structure.
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/FTId=VAR_005524.
04F9FC1F CRC32;
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the major protein
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PLEK_HUMAN Length: 350

February 14,

2000 08:02 Type:

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Q12535;

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ELIMINATIVE CLEAVAGE OF PECTIN TO GIVE
OLIGOSACCHARIDES WITH TERMINAL 4-DEOXY-6-METHYL-ALPHA-D-GALACT-
4-ENURONOSYL GROUPS.
-!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
-!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
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Eukaryota; Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Dothideales; Mycosphaerellaceae; Mycosphaerella.
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SIGNAL
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STRAIN-DSM 62763 / BERKELEY BLOXOM;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PECTIN LYASE PRECURSOR (EC 4.2.2.10)
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PROSITE; PS00800; PECTINESTERASE_1; 1.
PROSITE; PS00800; PECTINESTERASE_2; 1.
PRAM; PF01095; Pectinesterase; 1.
Hydrolase; Serine esterase; Cell wall; Signal.
Hydrolase; Serine asterase; Cell wall; Signal.
SIGNAL 1 1 7 BY SIMILARITY.
CHAIN 18 331 PECTINESTERASE.
SEQUENCE 331 AA; 35681 MW; C567C2B3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHRISTGAÚ S., KOFOD L.V., HALKIER T., ANDERSEN L.N., DORREICH K., DALBOGGE H., KAUPPINEN S.;
"Pectin methyl esterase from Aspergillus aculeatus: of cloning in yeast and characterization of the recombination of the combination of the recombination of the recombi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: INVOLVED IN MACERATION AND SOFT-ROTTING
-1- CATALYTIC ACTIVITY: PECTIN + N H(2)O - N METHANOL
-1- SIMILARITY: BELONGS TO THE PECTINESFERASE FAMILY.
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STINE REPRESENTATION OF THE REPRESENTATION O PME_ASPAC MVKSVLASAL FAVSALAASR TTAPSGAIVV AKSGGDYTTI GDAIDALSTS Length: 331 February 14, 2000 08:02 Type: ש Check: 2447

301 251 201 151 101 51 μ RASFAEKLDA KLTITDILGS DYTSWVDTSY SEYARVVFQQ VVEGPTSASI GYYGCNFTGY SYEDAGESDD LTATFRNKAV TIDIQIIFIE QDTLLAQTGN EGTYDEQVYL TSMTNVINSL TANGRSSETD GWTEWSTSTP TSYYVINKST VAAKEGDDVA QLYINSYIEG GSQVYNLNIA NTCGQACHQA PAMTGKVIIY GQTENTDSYA NTEYVTFGEY AVDFIFGQHA ANTGAGSEGT EGTYYLGRPW RAWFQNVDIR LALSAWADQQ DNLVTITHAI

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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PECTINESTERASE PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE)
                                                                                                                                                                                                                                                                        SEQUENCE 1.0
                                                                                                STRAIN-RH 5344;
MEDLINE; 90332436
                                                                                                                                               Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspe
                                                                                                                                                         Aspergillus tubingensis.
Eukaryota; Fungi: """"""
                                                                                                                                                                                                                                               PME_ASPTU
P17872;
                                 "Nucleotide and derived amino acid sequence isolated from Aspergillus niger strain RH 53 Nucleic Acids Res. 18:4262-4262(1990).
                                                                       KHANH N.Q., ALBRECHT JANY K.-D.;
                                                                                                                     SEQUENCE FROM N.A., AND
SEQUENCE FROM N.A. MEDLINE; 92039066.
                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                        PARTIAL
                                                                                    RUTTKOWSKI E.,
                                                                                                                        SEQUENCE
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RH 5344.
                                                                                      LOEFFLER F.,
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                                                                                      GOTTSCHALK M.,
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II AA_SEQUENCE 1.0
ID PSPB_BOVIN
AC P15781;
DT 01-ANG-1990 (F
DT 0
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SEQUENCE OF 1-10.

MEDLINE; 88025156.

YU S.-H., CHUNG W., OLAFSON R.W., HARDING P.G.R., POSSMAYER F.;

"Characterization of the small hydrophobic proteins associated pulmonary surfactant.";

Biochim. Biophys. Acta 921:437-448(1987).
                                                                                                                                                                                                                                                                  SEQUENCE.
SEQUENCE.
MEDLINE; 88077030.

OLAFSON R.W., RINK U., KIELLAND S.,
HARDING P.G.R., POSSMAYER E.;

HARDING P.G.R., POSSMAYER S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PULMONARY SURFACTANT-ASSOCIATED PROTEDLIPID SPL(PHE)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                             "Protein sequence analysis studies on the low molecular weight hydrophobic proteins associated with bovine pulmonary surfactant."; Biochem. Biophys. Res. Commun. 148:1406-1411(1987).
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EMBL; X54145; CAA38084.1; -.
EMBL; S14847; S10487
PIR; S10487; JT0589
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331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine esterase; Cell wall; Signal
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35715 MW;
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PTB_BACSU

Length: 299

February 14, 2000 08:02 Type:

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158

AVKLAAEHLS

ARFLLTGDSK LMKGNVPTSV

151 101

HAVGNNMPKA AALAAVETVN

AGNPDILLVP TIEAGNILY PKMEATVNAA ALAQMYKRGC 51

KLNELTSSMQ GHQVEIVHAN

TPEESAKLAV AHAEDEEVIR

RAVHHKTADV

VAVEDIPDED

MKLKDLIGKA SIHKNKTIAV

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IIAA_SEQUENCE 1.0

ID PTB_BACSU
AC P54530;
DT 01-0CT-1996 ()
DE BACLILUS SUBTILUS SU
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ALYCOLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-
CC LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES
THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINEWTONS
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBGELLAND LOCATION: EXTERCELLULAR.
CC -!- SUBCELLANDUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
CRESCHLANDOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
CRESCHLANDING STRACTENING SP-A AND SP-D) AND 2 SMALL
CC HYTOROPHOBIC PROTEINS (SP-B AND SP-C).
CRABOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
CC HYTOROPHOBIC PROTEINS (SP-B AND SP-C).
CRABOHYDRATE-BINDING GLYCOPROTEINS (SP-B AND SP-D)
R PIR; 802317; 802317.
SUSFACE film; Gaseous exchange.
SUSPECE FILM; Gaseous exchange.
SEQUENCE 79 AA; 8660 MW; 2B73807E CRC32;
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             EMBL; D84432; BAA12594.1; -.
EMBL; Z99116; CAB14340.1; -.
SUBTILIST; BG11722; YGIS.
PFAM; PF01515; PTA_PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=168 / JH642;

KOBAVASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,

SATO T., TAKEUCHI M.;

SUMMitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CATALYES THE CONVERSION OF BUTYRYL-COA THROUGH

-!- PHOSPHATE TO BUTYRATE.

-!- CATALYTIC ACTIVITY: BUTANOYL-COA + ORTHOPHOSPHATE = COA +

BUTANOYLPHOSPHATE.

-!- SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.

Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P54530;
01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
PROBABLE PHOSPHATE BUTYRYLTRANSFERASE (EC 2.3.1.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PHOSPHOTRANSBUTYRYLASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND
BUTYRYLTRANSFERASE FAMILY.
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            il protein;
299 AA; 3
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        n; Transferase; Acyltransferase
31772 MW; EF3F522D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGLRLRCSG
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AAVITGAKAP

IALTSRADSA ENKLYSIALA

ICASEEYTH

301

DESCMSOIDL

SLSKVVHKSF VEVNEEGTEA

AAATAAIMMM

RCARFVPRFC

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PTI6_HUMAN Length: 376
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01-FEB-1994 (Rel. 28, Lac
01-OCT-1996 (Rel. 34, Lac
PLACENTAL THROMBIN INHIB:
(PROTEASE INHIBITOR 6).
PIG OR PTI.
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PTI6_HUMAN
P35237;
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                                                                                                                                                                                                                                                              EMBL; 222658; CAA80373.1; -.
EMBL; 869272; AAB30320.1; -.
PIR; 835750; 835750
PIR; 448681; A48681.
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MORGENSTERN K.A., SI
CHING A., KISIEL W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94022386.
COUGHLIN P., SUN J., CERRUTI L.,
"Cloning and molecular character
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; C
Eutheria; Primates; Catarrhini;
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                                                                  101
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MIM; 17332
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                                                                                                                                                                                                                                PROSITE
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                                                                                        51
                                                                                                                                                                                   CONFLICT
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                                                                                                                                               E; PS00/26*, _____; 1.
PF00079; serpin; 1.
p; Serine protease inhibitor.
ITE 341 342 REACTI.
ITE 175 175 G -> E
LICT 175 362 R -> E
LICT 362 AA; 42587 MW; 2D8;
EKFVEWTRLD
                                           SPGSVDPLTR
                                                                                                                 MDVLAEANGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e proteinase inhibitor.";
Natl. Acad. Sci. U.S.A. 90:9417-9421(1993).
                                                                                         AQMAQILSEN
                                                                                                                                                                                                                    PF00079;
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MMDEEEVEVS LPRFKLEESY DMESVLRNLG MTDAFELGKA
                                            LVLVNAVYFR
                                                                                        KSGGGGDIHQ
                                                                                                               FALNLLKTLG
                                                                  QKFYQAEMEE
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28, Last sequence update)
34, Last annotation update)
N INHIBITOR (CYTOPLASMIC ANTIPROTEINASE) (CAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPRECHER C.A.,
                                                                                                                                     February 14, 2000 08:02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                            GNWDGQFDKE
                                                                                         GFQSLLTEVN
                                                                                                                 KDNSKNVFFS
                       LPYVGKELNM
                                                                  LDFISAVEKS
                                                                                                                                                            REACTIVE BOND.
G -> E (IN REF. 2).
R -> S (IN REF. 2).
; 2D806418 CRC32;
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                                                                                         KTGTQYLLRV
                       IIMLPDETTD
                                           NTEERLFKVS
                                                                  RKHINTWVAE
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                                                                  KTEGKIAELL
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I!AA_SEQUENCE I
ID PI18_HUMAN
AC P50452;
DT 01-OCT-19;
DT 01-OCT-19;
DT 01-OCT-19;
DT 01-NOV-19;
DN HOMO SAPI
OC Eutheria;
RN FISCHEAR
RT SCHRADER
RT MOLECHEAR
RT MOLECHEA
RT MOLECHEAR
RT MOL
AISSP; rvv--,
MIM; 601697; -,
PROSITE; PS00284; SERPIN; 1.
PFAM; PF00079; Serpin; 1.
Serpin; Serine protease inhibitor.
PSACTIVE BOND
39 340 REACTIVE BOND
39 37786 MW; 79AF74EC CRC
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SPRECHER C.A., MORGENSTERN K.A., MATHEWES S., DAHLEN J.R.,

SCHRADER S.K., FOSTER D.C., KISTEL W.;

"Molecular cloning, expression, and partial characterization of two novel members of the ovalbumin family of serine proteinase inhibitors.";

J. Biol. Chem. 270:29854-29861(1995).

--- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYTOPLASMIC ANTIPROTEINASE 2 (CAP2) (CAP-2) (PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                EMBL; L40377; AAC41939.1;
HSSP; P05619; 1HLE.
MIM; 601697; -.
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 AKFKMGYADE
                      GTVDPLTKLV
                                                                AAQMSQALCL
                                                                                    MDDLCEANGT
                                         FYQAELEELS
                                                              YKDGDIHRGF QSLLSEVNRT GTQYLLRTAN
                                                                                    FAISLFKILG
 VHTQVLELPY
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                     WNEQFDRKYT
 VEEELSMVIL
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                                                                                    EEDNSRNVFF SPMSISSALA MVFMGAKGST
                                           HINDWVAEKT
 LPDDNTDLAV
                      RGMLFKTNEE
                      KKTVQMMFKE
                                            EGKISEVLDA
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 VEKALTYEKE
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PTI8_HUMAN Length: 374

February 14, 2000 08:02 Type: P Check:

OND (BY SIMILARITY).

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SEEDHARD
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15-DEC-1999 (Rel. 39, Greated)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
PHOSPHORIBOSYLAMINOMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE
(SAICAR SYMTHETASE).
PURC OR MTH170.
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GMSTEKNVPL

SKVAHKCFVE KSKVQVFLPR

VNEEGTEAAA LKLEESYDLE

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PFLRRLGMID

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A ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,
A ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,
A JUNANI N., CANDON D., KEAGLE P., LUMM W., POTHIER B., QIU D.,
A JUNANI N., CARUSO A., BUSH D., SAFER H., PARWELL D., PRABHAKAR S.,
A MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
COMDIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
COMPLETE GENOME SEQUENCE OF METHADOBACTEATION THATMOGRAPHICUM
OF COMPLETE GENOME SEQUENCE OF METHADOBACTEATION THATMOGRAPHICS.";
L. J. BACTEATÓL 179:7135-7155(1997).
C. -- CATALYTIC ACTULTY: ATP + 1-(5-PHOSPHORIBOSYL)-4-CARBOXY-5-
AMIOIMIDADOLE + I-ASPARTATE ADP + ORTHOPHOSPHATE + 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)-5-AMINOIMIDAZOLE.
-- PATHAMY: SEVENTH STEP IN DE NOVO PORINE BIOSYNTHESIS.
C. -- SIMILARITY: BELONGS TO THE SAICAR SYNTHETASE FAMILY.
                                         SEQUENCE FROM N.A.
MEDLINE; 84119419.
SCHACHHAN H.K., PAUZA C.D., NAV
"Location of amino acid alterat
transcarbamoylase; Structural a
complementation";
Proc. Natl. Acad. Sci. U.S.A. 8
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                                                                                                                                                      Escherichia coli.
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P00479; Q47555;
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PROSITE; PS01057; SAICAR_SYNTHETASE_1;
PROSITE; PS01058; SAICAR_SYNTHETASE_2;
PFAM; PF01259; SAICAR_SYNT; 1.
    SEQUENCE FROM N.A. MEDLINE; 83195078.
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1-FEB-1995 (Rel. 31, Last sequence update)
5-JUL-1999 (Rel. 38, Last annotation update)
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haeota; Methanobacteriales;
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28244 MW;
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                                            81:115-119(1984)
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QIU D.,
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STRAIRE 22 / MG1655;

MEDLINE 97426617.

BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE: 95334362
BURLAND V.D., PLUNKETT G
BLATTNER F.R.;
BLATTNER F.R.;
"Analysis of the Escheri
region from 92.8 through
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SEQUENCE OF 1-53 FROM N.A.
MEDLINE; 89017155.
MEDLINE; 89017155.
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ROLAND K.L., LIU C., TURNBOUGH C.L. JR.;
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TROLE Of the ribosome in suppressing transcriptional the pyrBI attenuator of Escherichia coli K-12.";
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PASQUALI C., SANCHEZ
FRUTIGER S., PAQUET 1
HOCHSTRASSER D.F.;
                                                                                                                                   MEDLINE; 91035438.

DONABUE J.P., TURNBOUGH C.L. JR.;

Characterization of transcriptional initiation f
P2 of the pyrBI operon of Escherichia coli K12.";

J. Biol. Chem. 265:19091-19099(1990).
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MEDLINE; 83169660.
TURNBOUGH C.L. JR.
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Proc. Natl. Acad. Sci. U.S.A. 80:2467-2471(1983).
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coli.";
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                                                                                                                                                                                                                                               Proc. Natl.
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nce 277:1453-1474(1997).
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      EMG2;
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                                                                     F., GOLAZ O.,
APPEL R.D.,
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[12]
SEQUENCE OF 1-5.
STRAIN-K12 / W3110;
MEDLINE; 98291876.
MOLLOY M.P., HERBERT B.R., WALSH B.J., TYLER M.I., TRAINI M.,
SANCHEZ J.-C., HOCHSTRASSER D.F., WILLIAMS K.L., GOOLEY A.A.;
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separation using two-dimensional gel electrophoresis.";
selectrophoresis 19:837-844(1998).
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Structure of unligated aspartate carbamoyltransferase coli at 2.6-A resolution.";

Proc. Natl. Acad. Sci. U.S.A. 81:4037-4040(1984).
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"Comparing the predicted and observed in the genome of Escherichia coli K-12 Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE; 91104727.
MEDLINE; 91104727.
STEVENS R.C., GOUAUX J.E., LIPSCOMB W.N.;
"Structural consequences of effector binding to the T state of
"Structural consequences of effector binding to the Unligated aspartate carbamoyltransferase: crystal structures of the unligated and ATP- and CTP-complexed enzymes at 2.6-A resolution.";
Bischemistry 29:7691-7701(1990).
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X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).

GOUAUX J.E., STEVENS R.C., LIPSCOMB W.N.;

COUAUX J.E., STEVENS R.C., LIPSCOMB W.N.;

Phosphonoacetamide, malonate, and CTP or ATP at 2.8-A resolution and phosphonoacetamide, malonate, and CTP or ATP at 2.8-A resolution and
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L; J01670; AAA2474.1; -.
L; J014003; AAA97142.1; -.
L; AE000495; AAC7202.1; -.
L; M60508; AAA24481.1; -.
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A00561; 1ACM; 1ACM; 1ATC; 1ATC

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HELIX SEQUENCE

285 310 AA;

304 34296 MW;

BDF9E927 CRC32;

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I!AA_SEQUENCE 1.0

IIAA_SEQUENCE 1.0

PYRB MYCTU
AC p71808;

OT 01-NOV-1997 (F
DT 01-NOV-199 (F
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SEQUENCE S.T., 
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence.";

Nature 393:537-544(1998);
-!- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE
ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE
-!- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                       EMBL; 281011; CAB02641.1; -. HSSP: PO0479; 3AT1. PROSITIE; PS00097; CARBAMOXLTRANSFERASE; PFAM; PF00185; OTCace; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1
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PYRB OR RV1380 OR MTCY02B12.14.
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          Length: 319
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                                                           biosynthesis; Transferase.
319 AA; 33818 MW; 38CF9A86 CRC32;
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2.1.3.2) (ASPARTATE
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Type: P Check: 1547
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ADALIIRHPA FYENSTRTRV MTPRHLLTAA

SGAAHLLAQW TGAHNDGPAV INAGDGTHEH PTQALLDALT

SSVGKGESLR DTALTLRAAG

IIAA_SEQUENCE 1.0
ID PERB_PERHO
AC O58451;
DT 15-DEC-1999 (F
DT 15-DEC-1999 (F
DT 15-DEC-1999 (F
DT 15-DEC-1995 (F

301 251 201 151 101

LALVLGVI NLKVLEKAKD ELREKGMKVV GRIDGLKIGL CDVIVIRHPK

ELRIMHPLPR VDEIHPEVDN TKHAIYFRQV

ETTTLEDVIG LGDLKYGRTV

KLDVLYVTRI HSLAEALTFY AEVPVINAGD

QKERFPDEQE DVELYLISPE GSNQHPTQTL

LLRMPRHIVE LDLYTIKKEF

PYRB_YYHO STANDARD; PRT; 308 AA O58451; 05-DEC-1999 (Rel. 39, Created) 15-DEC-1999 (Rel. 39, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation update) ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2)

10n update)
2.1.3.2) (ASPARTATE

PYRB_PYRAB

Length: 308

February 14, 2000 08:02 Type: P Check:

9304

7CEC7D77 CRC32;

51

FFEPSTRTRL SFESAMHRLG GAVIGFAEAS TSSVKKGESL RDTIKTVEQY MDWKGRDVIS IRDFSKEDIE TVLATAERLE RELKEKGQLE YAKGKILATL

EGAARLAAEV

51

SFEVAGKWMS

DLSRDDATAI LDDADRFAQA LVGRDIKKLP TLRGRTVVTM

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X MEDLINE; 97352668.

A PURCAREA C., HERVE G., LADJINI M.M., CUNIN R.;

T ASPATTATE transcarbamylase from the deep-sea hyperthermophilic rareases pyrococcus abyss: genetic organization, structure, and structure, and structure.

RT archaeon Pyrococcus abyss: genetic organization, structure, and structure.

RT expression in Escherichia coli."

RI J. Bacteriol. 179.4143-4157(1997).

CC -!- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE = CRIALYTIC ACTIVITY - CARBAMOYL-PHOSPHATE + N-CARBAMOYL-PHOSPHATE BIOSYNTHESIS.

CC -!- SUBUNIT: CONTAINS CATALYTIC AND REGULATORY CHAINS.

CC -!- SUBUNIT: CONTAINS CATALYTIC AND REGULATORY CHAINS.

CC -!- SUBUNIT: CONTAINS CATALYTIC AND REGULATORY CHAINS.

CC -!- SUBUNIT: SELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PROSITE; PS00097; CARBAMOYLTRANSFERAS
PFAM; PF00185; OTCace; 1.
Pyrinidine biosynthesis; Transferase.
SEQUENCE 308 AA; 34901 MW; 7CEC71
                                                                EMBL; U61765; AAB62984.1; -.
HSSP; P00479; 3AT1.
PROSITE; PS00097; CARBAMOYLT
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Archaea; Euryarchaeota;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2) (ASPARTATE TRANSCARBAMYLASE) (ATCASE).
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                                                            CARBAMOYLTRANSFERASE; 1
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PYRB_PYRHO
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01-AUG-1988 (Rel. 08, Created)
01-AUG-1991 (Rel. 17, Last seguence update)
01-FEB-1991 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLIRANSFERASE CATALYTIC CHAI
TRANSCARBAMYLASE) (ATCASE).
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STRAIN-LIL,
MEDLINE, 87246692.
MICHAELS G., KELLN R.A., NARGANG F
"Cloning, nucleotide sequence and
Salmonella typhimurium LT2.";
Riochem. 166:55-61(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; APO00003; BAA29811.1; -.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
PFAM; PF00185; OTCace; 1.
Pyriniddine biosynthesis; Transferase.
SEQUENCE 308 AA; 34862 MW; 12633B0D CR
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PYRB_SALTY
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YAMAMOTO S., SEKINE M., BABA S., KOSGI H., HOSOYAMA A., NAGAI Y.,
YAMAMOTO S., OGURA K., OTSUKA R., NAKAZAWA H., TAKAMITA M., OGEUKI Y.,
YAMAMA M., TAKAMITA M., OGUCHI
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
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Archaea; Euryarchaeota;
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PYRB OR PH0720.
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                                                                                    SEQUENCE FROM N.A.
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                                                                                                                        Proteobacteria;
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2 MW; 12633B0D CRC32;
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                                                                                                                        Enterobacteriaceae
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PYRB_SALTY Length: 310
                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BECK D, KEDZIE K.M., WILD J.R.;

"Comparison of the aspartate transcarbamoylases from Serratia marcescens and Escherichia coli.";

J. Biol. Chem. 264:16629-16637(1989).

-1- CAPALYTIC ACTIVITY: CARBANOYL-PHOSPHATE + ASPARTATE = ORTHOPIOSPHATE + N-CARBANOYLASPARTATE.

-1- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.

-1- PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.

-1- SUBUNIT: HETERODDECAMER (23::R2) OF SIX REGULATORY PYRI CHAINS ORGANIZED AS THREE DIMERS (R2).

ORGANIZED AS THREE DIMERS (R2).
                                                                                                                                                                                                                                                                                                   Bacteria;
Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X05641; CAA29129.1;
PIR; S00049; OWEBAC.
HSSP; P00479; 1RAG.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                        01-FEE-1991 (Rel. 17, Created)
01-FEE-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN
TRANSCARBAMYLASE) (ATCASE).
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PROSITE; PS00097; CARBAMOYLTRANSFERASE;
PFAM; PF00185; OTCace; 1.
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NIT_MET 0 0 BY SIMII
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PATHWAY: SECOND STEP IN PYRIMIDINE BIOSYNTHESIS.
SUBUNIT: HETERODODECAMER (2C3:3R2) OF SIX CATALYTIC ORGANIZED AS TWO TRIMERS (C3), AND SIX REGULATORY PY ORGANIZED AS THREE DIMERS (R2).
SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                               SIMILARITY: BELONGS TO THE ATCASES/OTCASES
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                                                                                                                                                                                                                                                                                                                                Proteobacteria;
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                                                                                                                                                                                                                                                                                                                              gamma subdivision;
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                                                                                   FAMILY.
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PYRB_VIBS2 Length: 310 February 14, 2000 08:02
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PYRB_VIBS2
P96174;
                                   EMBL; Y09786; CAA70923.1; -.
HSSP; P00479; IRAG.; CARBAMOYLTRANSFERASE; 1.
PFAM; PF00185; OTCace; 1.
PYTINIGINE blosynthesis; Transferase.
SEQUENCE 310 AA; 34419 MW; C460D24E CR
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         VAN DE CASTELLE M., LIANG Z., FENG Z.Y., LEGRAIN C., GLANSDORFF N.;
SUBMITTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE =
-!- ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
-!- PATHWAY: SECOND STEP IN PYKIMIDINE BIOSYNTHESIS.
-!- PATHWAY: SECOND STEP IN PYKIMIDINE BIOSYNTHESIS.
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                                                                                                                                                                                                                                                                                       SIMILARITY).
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
[1]
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE CATALYTIC CHAIN
TRANSCARBAMYLASE) (ATCASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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INIT_MET 0 0 BY SIMII
SEQUENCE 305 AA; 33240 MW; 3E4D88
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                                     C460D24E CRC32;
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DAFVMRHPQE GAARLASEFS NVPVINGGDG

SNOHPTOTLL

DLFSIYETQG

EASTRIRLSF ETAIQRLGGT VIGFDNASNT SLAKKGETLA DSISVISSYV

51

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MANPLFRKHI

VSINDISRNE

LELIVKTAAK LKKQPQPELL

KNKVIASCFF

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IIAA_SEQUENCE 1.0
ID RA51_DROME
AC Q27297;
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ID PYRZ_BACSU
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KAHLER A.E., SWITZER R.L.;

KAHLER A.E., SWITZER R.L.;

RAHLER A.E., SWITZER R.L.;

ROUTH IN SUBILIZED FOR dihydroorotate dihydrogenase activity in Baccilius subtilis."

J. Bacctriol. 178.5013-5016(1996).

-I. FUNCTION. PROBABLE ELECTRON CARRIER PROTEIN INVOLVED IN THE TRANSFER OF REDUCING EQUIVALENTS FROM THE FLAVOPROTEIN SUBUNIT THE ELECTRON TRANSPORT SYSTEM IN THE CELL MEMBRANE.

-I. PANTHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.

-I. SIMILARITY: TO S. TYPHIMURIUM ASRB AND P. FURIOSUS HYDG.
                                                                       251
                                                                                                      201
                                                                                                                                        151
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                                                                                                                                                                                                                                                                                                      EMBL; M59757; AAA21271.1; -.
EMBL; Z99112; CAB13427.1; -.
PIR; G39845; G39845.
SUBTILIST; BG10717; PYRDII.
Pyrimidine biosynthesis; Electron transport.
Pyrimidine biosynthesis; S164078 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Functional organization and nucleotide sequence of the Bacillus subtilis syrimidine biosynthetic operon.";
J. Biol. Chem. 266:9113-9127(1991).
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Bacillus subtills:
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p25983;
01.MAY-1992 (Rel. 22, Created)
01.MAY-1992 (Rel. 22, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
DIHYDROOROTATE DEHYDROGENASE ELECTRON TRANS
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                   STANDARD;
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                                                                                                                                                                                                       RVDGEGTRLL
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                   PRT;
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IIAA_SEQUENCE 1.0

ID RBCK_CHRVI STANDARD; PRT;
AC P25544;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence)
DT 01-MAY-1992 (Rel. 22, Last annota)
Therefore the company of the c
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STRAIN-CANTON-S;
STRAIN-CANTON-S;
MEDLINE; 95161094.
AKABOSHI E., INOUE Y., RYO H.;
"Cloning of the cDNA and genomic DNA gene of Drosophila melanogaster.";
Jpn. J. Genet. 69:663-670(1994).
[2]
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01-NOV-1997 (Rel. 35
15-DEC-1999 (Rel. 35
DNA REPAIR PROTEIN F
RAD51 OR DMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96207535.

MCKEE B.D., REN X.J., HONG C.S.;

"A recA-like gene in Drosophila melanogaster that is en in the control of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLYBASE; FBgn
DNA-binding;
NP_BIND 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D37788; BAA07039.1; -. EMBL; D17726; BAA04580.1; -. EMBL; L41342; AAA64873.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   Chromatium vinosum
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1342; AAA64873.1;
FBgn0011700; Rad51.
ding; ATP-binding; Nuclear protein.
ATP (POTENTIAL).
1724 131 ATP (BD6F6D2 CRC32;
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35, Last sequence update)
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N RAD51 HOMOLOG (RECA PROTEIN
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EMBL; M26396; -; NOT_ANNOTATED_CDS.
EMBL; M26396; -; NOT_ANNOTATED_CDS.
PIR, A40369; A40369.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
PFAM; PF00126; HTH_L; 1.
PFAM; PF00126; HTH_L; 1.
DNA_BIND 20 39 H-T-H MOTIF (BY SIMILARITY).
DNA_BIND 20 39 H-T-H MOTIF (BY SIMILARITY).
TOWNSHIP 302 AA; 34092 MW; CA38CF20 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VILLE A.M., KOBAKASHI H., AKAZAWA T.;

VILLE A.M., KOBAKASHI H., AKAZAWA T.;

"Expressed genes for plant-type ribulose 1,5-bisphosphate
carboxylase/oxygenase in the photosynthetic bacterium Chromatium
vinosum, which possesses two complete sets of the genes.";

J. Bacteriol. 171:2391-2400(1989).

-i- FUNCTION: TRANS-ACTING TRANSCRIPTIONAL REGULATOR OF RUBISCO
GENES (RECAB) EXPRESSION.

-i- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
                                                                                                      P10647;
Ol-JUL-1989 (Rel. 11, Created)
Ol-JUL-1989 (Rel. 11, Last sequence update)
Ol-JUL-1989 (Rel. 37, Last annotation update)
IS-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(EC 4.11.39) (RUBISCO SMALL SUBUNIT C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIALE A.M. KOBAYASHI H., AKAZAWA T., HENIKOFE S.;
"rbcR, a gene coding for a member of the LysR family of
transcriptional regulators, is located upstream of the er
of ribulose 1,5-bisphosphate carboxylase/oxygenase genes
photosynthetic bacterium Chromatium vinosum.";
3, Bacteriol. 173:5224-5229(1991)
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MEDLINE; 91317745.
VIALE A.M., KOBAYASHI
                                            euphyllophytes;
core eudicots;
                                                                                                                                                                                                                                                                       301
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                                            Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons
core eudicots; Asteridae; euasterids I; Solanales; Solanacea
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                                                Solanaceae;
                                                                                Tracheophyta;
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SEQUENCE Solanum.

FROM

N.A.

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RANGE OF THE REPORT OF THE REP
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                                                                                      SEQUENCE FROM N.A. STRAIN=CV. VF36; MEDLINE; 87163513. MCKNIGHT T.D., ALEX
                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT 1) (LESS17).
RBCS-1.
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ACTIVE SITE.

CAPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-PHOSPHO-D-GLYCERATE.

1 CAPALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.

1- SUBCELLUAR LOCATION: CHLOROPLAST.

1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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MEDLINE; 88124937.

WOLTER F.P., FRITZ C.C., WILLMITZER L., SCHELL J., SCHREIER P.H.;

"IDCS genes in Solanum tuberosum: conservation of transit peptide and

"IDCS genes in Solanum tuberosum: conservation of transit peptide and

"IDCS genes in Solanum tuberosum: conservation of transit peptide and

"IDCS genes in Solanum tuberosum: conservation of transit Acad. Sci. U.S. A. 85:846-850(1988).

PICOC. Natl. Acad. Sci. U.S. A. 85:846-850(1988).

"IDCA FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF

"ID-RIBULOSE 1.5-BISSHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNVHETICO

CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAMENINATION OF

THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH

REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME

ACTIVE STEE
                                                                                                                                                                                                                   Lycopersicon esculentum (Tomato).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;

solanum.

[1]
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MENDEL; 15074; SOLtu;rbcS;mn15074.
MENDEL; 15074; SOLtu;rbcS;mn15074.
PFAM; PF00101; RubisCO_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03613; AAA33838.1; -. PIR; A31083; RKPOSC. HSSP; P00866; IRLC.
                         MCKNIGHT T.D., ALEXANDER D.C., BABCOCK M.S., SIMPSON R.I "Nucleotide sequence and molecular evolution of two tome encoding the small subunit of ribulose-1,5-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWPPINMKKY ETLSYLPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VATRSNVAQA SMVAPFTGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REHNSSPGYY DGRYWTMWKL
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181
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                                                                                                                                                                                      17).
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RIBULOSE BISPHOSPHATE CARBO
CHAIN C.
; 44574D48 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                tomato
                                                                                             R.B.;
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RBS1_LYCES
                           CONFLICT
                                                                                                              EMBL; M15235; AAA34191.1; -.
EMBL; M13542; AAA34188.1; -.
EMBL; M13542; AAA2400.1; -.
EMBL; X05982; CAA46868.1; -.
EMBL; X05964; RKTOS1.
HSSP; P00866; IRLC.
HSSP; P00866; IRLC.
BFAM; PF00101; RuBisCO_small; 1.
PFAM; PF00101; RuBisCO_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration; Photosynthesis; Carbon dioxide fixation; Chloroplast; Transit
                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    "Developmental and organ specific changes in DNA-protein interactions in the tomato rbcS1, rbcS2 and rbcS3A promoter regions.";

Plant Mol. Biol. 21:69-88(1993)

-i- FUNCTION: RUBISCO CARALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBUIOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, WELL AS THE OXIDATIVE FRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-20 FROM N.A. (RBCS-1).
STRAIN-CV. VENT CHERRY LA1221; TISSUE-ROOT;
MEDLINE; 93144693.
MANZARA T., CARRASCO P., GRUISSEM W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUGITA M., MANZARA T., PICHERSKY E., CASHMORE A., GRUISSEM W.; "Genomic organization, sequence analysis and expression of all genes encoding the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase from tomato.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PICHERSKY E., BERNATZKY R., TANKSLEY S.D., CASHMORE A.R.; "Evidence for selection as a mechanism in the concerted ev Lycopersicon esculentum (tomato) genes encoding the small ribulose-1,5-bisphosphate carboxylase/oxygenase."; Proc. Natl. Acad. Sci. U.S.A. 83:3880-3884(1986).
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Gen. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
 Length: 181
                                                                                                     family.
                               181 AA;
                                            79
                                                                        58
181
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 February 14,
                             79
20307
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                               MW;
                                         CHLOROPLAST (BY SIMILA RIBULOSE BISPHOSPHATE CHAIN 1.
                             981E9B5C CRC32;
 2000
08:02
                                                                                         (BY SIMILARITY
 ש
                                                                           CARBOXYLASE SMALL
 Check:
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MASSIVSSAA AATRSNVAQA SMVAPFTGLK SAASFPVTKK NNNVDITSLA

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- SNGGRVRCMQ VWPPINMKKY ETLSYLPDLS DEQLLSEIEY LLKNGWVPO
- 101 EFETERGFVY RENNSSPGYY DGRYWTMWKL PMFGCTDATQ VLAEVQEAKK
- 51 AYPQAWVRII GFDNVRQVQC ISFIAYKPEG F

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OF THE SERVICE OF SERV
!!AA_SEQUENCE 1.0 ST.
ID RBS1_SOLTU ST.
AC P26574;
DT 01-AUG-1992 (Rel.
                                                                                                                                                                                                                                                                                                      RBS1_PETSP Length: 180
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RBS1_PETSP
P04714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
TUMER N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit Multigene family.

1 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X03820; CAA27444.1; -. PIR; A24917; RKPJS8. HSSP; P00866; IRLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petunia sp. (Petunia).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(EC 4.1.1.39) (RUBISCO SMALL SUBUNIT SSU8).
                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLULAR LOCATION: CHLOROPLAST.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVE SITE.
CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE +
2 3-PHOSPHO-D-GLYCERATE.
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                                                                                                                    YPNAWIRIIG
                                                                                                                                                            FETEHGFVYR
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                                             STANDARD;
                                                                                                                                                                                                                WPPYGKKKYE
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  23, Created)
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180
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                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                 SFIAYKPPGF
                                                                                                                                                                                                                TLSYLPDLTD
                                                                                                                                                                                                                                                        SMVAPFNGLK
                                                                                                                                                               GRYWTMWKLP
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RIBULOSE BISPHOSPHATE CARBC
CHAIN SSUB.
; 71E5C2F3 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIRONAKA C.M.,
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ID RBS2_LYCES
AC P07179;
DT 01-APR-1988 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGURNCE FROM N.A.

STRAIN-CV. AM 80.5793;

FRITZ C.C., WOLTER F.P., SCHENKEMEYER V., HERGET T., SCHREIER P.H.;

FRITZ C.C., WOLTER F.P., SCHENKEMEYER V., HERGET T., SCHREIER P.H.;

SUBMILTED (DEC-1992) to the EMBL/GenBank/DDBJ databases.

SUBMILTED (DEC-1992) to the EMBL/GenBank/DDBJ databases.

FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION THE PRIMARY EVENT IN THE PHOTORESPIRATION PROCESS. BOTH THE PRIMARS SCHEDUS SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
(EC 4.1.1.39) (RUBISCO SMALL SUBUNIT 1).
RBCS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88124937.

WOLTER F.P., FRITZ C.C., WILLMITZER L., SCHELL, WOLTER F.P., FRITZ C.C., WILLMITZER L., SCHELL, "rbcs genes in Solanum tuberosum; conservation exon shuffling during evolution."; exon shuffling during evolution."; Proc. Natl. Acad. Sci. U.S.A. 85:846-850(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                         101
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                        151
                                                                                                                                                                                                                                                                                                                                        Lyase; Oxi
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B31083; RKPOS1.
PIR; S31497; S31497.
HSSP; P00866; 1RLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X69759; CAA49413.1; -.
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                                                                                                                                                                                                                                                                                                                                                         MENDEL; 490; SOLtu;rbcS;l.

PRAM; PRO0101; RuBLSCO_small; 1.

Photosynthesis; Carbon dioxide fixation; Photorespiration; Photosynthesis; Carbon dioxide fixation; Chloroplast; Transit Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
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                                                                                                                                                             51
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ACTIVE SITE.
- CATALYTIC ACTIVIT
2 3-PHOSPHO-D-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2)
3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLATE.
SUBUNIT: B LARGE CHAINS + 8 SMALL CHAINS.
SUBCELLUTAR LOCATION: CHLOROPLAST.
SUBCELLUTAR LOCATION: THE RUBISCO SMALL CHAIN FAMILY.
SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                        SYPOAWIRII
                                                                                                                                                             SNGGRVRCMQ
                                                                                                                                                                                                MASSVISSAA
                                                                                                                         EFETEHGFVY
                                                                                                                                                                                                                                                                                                                                                                                                                                 P00866;
                                                                                                                                                                                                                                 Length: 181
                                                                                                                                                                                                                                                                                                                                          family.
                                                                                                                                                                                                                                                                    181 AA;
  (Rel.
                                                                                                                                                                                                                                                                                                         59
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                                       STANDARD;
                                                                                                                                                                                                VATRTNVTQA
                                                                                        GFDNVRQVQC
                                                                                                                           RENHKSPGYY
                                                                                                                                                             VWPPINMKKY
                                                                                                                                                                                                                                                                                                         58
181
                                                                                                                                                                                                                                 February 14, 2000
                                                                                                                                                                                                                                                                      20556
                                                                                                                                                                                                                                                                      MW;
                                                                                          ISFIAYKPEG
                                                                                                                         DGRYWTMWKL
                                                                                                                                                             ETLSYLPDLT
                                                                                                                                                                                                GSMIAPFTGL
                                                                                                                                                                                                                                                                                  CHLOROPLAST (BY SIMILARITY).
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
CHAIN 1.
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                                                                                                                           PMFGCTDATQ
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                                                                                                                                                                                                                                                                      CRC32;
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                                                                                                                              VLAEVQECKE
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transit peptide
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RC STRAIN-CV. VENT CHERRY LA1221; TISSUE-ROOT;

RX MEDILINE; 93144693.

RA MANZARA T. (CARRASCO P., GRUISSEM W.;

RT "Developmental and organ-specific changes in DNA-protein interactions RT in the Comato rbc51, rbc52 and rbc53A promoter regions.";

Plant Mol. Balol. 21:69-88(1993).

CC -i. FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARRASCO OF CO PRIBULOSE 1,5-BISHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC CO CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRACENTATION OF CC THE PENTOSE SUBSTRATE IN THE PHOTORESPITATION PROCESS. BOTH CC REACTIONS OCCUR SIMULIANDOUSLY AND IN COMPETITION AT THE SAME CC ACTIVE SITE.

CC -1. CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = CHALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = CHALYTIC ACTIVITY: B-RIBULOSE 1,5-BISPHOSPHATE + O(2) = CHALYTIC ACTIVITY: B-RIBULOSE 1,5-BISPHOSPHATE + O(2) = CHALYTIC ACTIVITY: B-RIBULOSE 1,5-BISPHOSPHATE + O(2) = CHALYTIC ACTIVITY: B-CHAINS + 8 SMALL CHAINS - COURSELLAR LOCATION: CHLOROPLAST.

CC -I. SUBCLILLAR LOCATION: CHLOROPLAST.

CC -I. SUBCLILLAR LOCATION: CHLOROPLAST.
      01-NOV-1990 (Rel. 16, La
15-JUL-1999 (Rel. 38, La
RIBULOSE BISPHOSPHATE CA
(EC 4.11.39) (RUBISCO S
RBCS-2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS.
MANZARA T.
                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGITA M., MANZARA T., PICHERSKY E., CASHMORE A., GRUISSEM W., "Genomic organization, sequence analysis and expression of all genes encoding the small subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase from tomato.";
Mol. Gen. Genet. 209:247-256(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PICHERSKY E., BERNAMZKY R., TANKSLEY S.D., CASHMORE A.R.;
"Evidence for selection as a mechanism in the concerted evidence for selection as a mechanism in the concerted evidence for selection (tomato) genes encoding the small ribulose-1,5-bisphosphate carboxylase/oxygenase.";
Proc. Natl. Acad. Sci. U.S.A. 83:3880-3884(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxylase.";
Gene 48:23-32(1986).
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MCKNIGHT T.D., ALEXANDER D.C., BABCOCK M.S., SIMPSON R.B.;

"Nucleotide sequence and molecular evolution of two tomato
encoding the small subunit of ribulose-1,5-bisphosphate
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Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;

core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-9 FROM
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M15236; AAA34192.1; -. M13543; AAA34189.1; -. X05983; CAA29401.2; -.
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CHERRY LA1221; TISSUE=ROOT;
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CHERRY LA1221;
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Last annotation update)
CARBOXYLASE SMALL CHAIN:
O SMALL SUBUNIT 2A) (LESS
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all
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01-0CT-1993 (Rel. 27, La
01-0CT-1993 (Rel. 27, La
15-DEC-1998 (Rel. 37, La
RIBULOSE BISHOSPHATE CA
(EC 4-11.139) (RUBISCO S
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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TRANSIT
                       PIR; S31498; S31498.
HSSP; P00866; 1RLC.
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                                                EMBL; X69763; CAA49417.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytas; spermatophyta; Magnoliophyta; eudicotyledons;
euphyllophytas; Asteridae; euasterids I; Solanales; Solanaceae;
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PIR; S02363; RKTOS2.
HSSP, P00866; IRLC.
HSSP, P00866; IRLC.
HSNDEL; 414; LYCes; PDCS; 2.
PFAM; PF00101; RuBisCO_small; 1.
PFAM; PF00101; RuBisCO_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration; Photosynthesis; Carbon dioxide fixation; Chloroplast; Transit Lyase; Oxidoreductase; Monooxygenase; Chloroplast; Transit
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ACTIVE SITE.

CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-PHOSPHO-D-GLYCERATE.

CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

SUBCELLULAR LOCATION: CHLOROPLAST.

SUBCELLULAR LOCATION: CHLOROPLAST.

SUBCELLULAR LOCATION: THE RUBISCO SMALL CHAIN FAMILY.

SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
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CARBOXYLASE SMALL CHAIN 3
O SMALL SUBUNIT 3).
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W: 6BE7042D CRC32;
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MENDEL; 4>0,

SOLtu; rbcS; 6 RuBisCO_small;

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SOFFICKW
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PUTATIVE RIBOKINASE (EC 2.7.1.15).
SPBC16G5.02C.
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 301
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                                                                                                                                                                                 PFAM; PF00294; pfkB; 1.
Hypothetical protein; T
SEQUENCE 318 AA; 332
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                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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TRANSIT
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33250 MW; D40648BF CRC32;
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Monooxygenase; Chloroplast;
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                      SIAHGQPLKD
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RIBULOSE BISPHOSPHATE CARBO
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loroplast; Transit
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ID RBS_MUSAC

PRT;

180

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RBS_MUSAC
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN
(RUBISCO SMALL SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Musa acuminata (Banana).
Musa acuminata (Banana).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida;
7inniberales; Musaceae; Musa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 3-PHOSPHO-D-GLYCERATE.

1 CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.

1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.

1- SUBCELLULAR LOCATION: CHLOROPLAST.

1- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGEV I., KHAYAT E., GEPSTEIN S.;
Submitted (JUN-1997) to the EMBLYGENEARK/DDBJ databases.
-i- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSEVATION CARBON DIOXIDE FIXATION. AS WELL AS THE OXIDATIVE PRAGMENTATION CARBON DIOXIDE FIXATION. AS WELL AS THE OXIDATIVE PRAGMENTATION OF THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                       SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF008214; AAB63287.1; -1
FPAM; FP00101; RubisCo_small; 1.
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Photosynthesis; Carbon dioxide fixation; Photorespiration;
Lysse; Oxidoreductase; Monooxygenase; Chloroplast; Transit peptide.
TRANSIT 1 58
CHLOROPLAST (BY SIMILARITY).
TRANSIT 1 58
RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL
                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                              101
SEQUENCE FROM N.A.
STRAIN=CANTON-S; TISSUE-HEAD
MEDLINE; 96203080.
                                                                 Ephydroidea;
                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata: H
Pterygota: Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat)
RHYTHMICALLY EXPRESSED GENE 5 PROTEIN (DREG
                                                                                                                                               REG-
                                                                                                                                                                                                                                                                                                                                                                               51
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                                                                                                                                                                                                                                                                                                                                                                                                                   Ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVE SITE CATALYTIC A
                                                                                                                                                                                                                                                                                                            YPHAFIRIIG
                                                                                                                                                                                                                                                                                                                                                                                                                   MVSSMMVSSA ATFTRASPAQ SSMVAPFTGL KSASAFPVTR KPNADLSHLF
                                                                                                                                                                                                                                                                                                                                                                               SNGGRVQCMK
                                                                                                                                                                                                                                                                                                                                                EFCPKGFVWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) =
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                ENHRSPGYYD
                                                                                                                                                                                                                                                                                                                                                                               VWPIEGVKKF
                                                                                                                                                                                                                                                                                                            FDNNRQVQCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     February 14, 2000 08:02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20511 MW;
                                                                                                                                                                                                                                                                                                                                              GRYWTMWKLP MFGCTDAVQV AKEVEECKKE
                                                                                                                                                                                                                                                                                                            SFIAYKPTGY
                                                                                                                                                                                                                                                                                                                                                                               ETLSYLPTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                              protein (DREG-5)
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3BB9BCBD CRC32;
                                                                                                                                                                                                                                                       298 AA
                                                                                                                                                                                                                                                                                                                                                                                 DEALVKQIEY LLRSKWIPCL
                                                                                                         Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type:
                                                                                          Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Check:
                                                                                          Muscomorpha
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REG5_DROME Length: 298
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                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                EMBL; U40818; AAA83758.1; -. HSSP; P30041; 1PRX. PF0AM; PF00578; AhpC-TSA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"A novel circadianly expressed Drosophila melanogaster gene dependent on the period gene for its rhythmic expression.";

EMBO J. 15:1625-1631(1996).

-!- FUNCTION: INVOLVED IN THE GENERATION OF BIOLOGICAL RHYTHMS
-!- FUNCTION: INVOLVED IN THE GENERATION OF BIOLOGICAL RHYTHMS
-!- FUNCTION: INVOLVED IN THE HEAD, OSCILLATES IN ABUNDANCE WITH A DAILY PEAK DURING EARLY NIGHT, EYEN UNDER CONSTANT DARKNESS. OSCILLATION
IS DEPENDENT ON PERIOD (PER) FUNCTION.

-!- TISSUE SPECIFICITY: EXPRESSED IN HEAD, BUT NOT IN THE BODY.
-!- TISSUE SPECIFICITY: EXPRESSED IN 24 HOURS EMBRYO.
Antioxidant.
218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-STAR MOSS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tortula ruralis (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Bryidae; Pottiales; Pottiaceae; Tortula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biological rhythms.
DOMAIN 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEHYDRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVHCKSTAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSGASLVTTR QPLQQPLPTP PASSLIILTR
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T H.B. II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34, Created)34, Last sequence update)37, Last annotation update)
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                24084 MW;
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                ADFD8F42 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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II AA_SEQUENCE 1.0
ID REBB_NEIGO
AC P37761;
DT 01-0CT-1994 (R
DT 01-0CT-1996 (R
DT 01-DT-1996 (R
DE DTDF-GLUCOSE 4
GN REBB.
GN REBB.
OS Neisseria gono

4 (Rel. 30, Created 4 (Rel. 30, Last sec 5 (Rel. 34, Last and SE 4,6-DEHYDRATASE

annotation update)

Created)

Neisseria gonorrhoeae.

151

CTQLLVPPAP FNSFNELAAE

101

IGNGMLSSQE ASQAAIDLML

51

LTTGRPYGLD

DSSAEVILPA AKMVKERFDS

201

LFIPESLKDI ATEMLMRKMD

251

RSRDTNARGA YKLQNTITEG

PKAVPTKKRR VATRVRGRKS

NRLQQKKSEL TEEDVMKLVS QNNKLLDNRK SSAEDSSVSS

EGRTEVNHAN VVTQLLTLVP QLYKSIAIII

> PDRQAALIGD GRUPEKDKKF

STANDARD;

346

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REP2_YEAST
                                                      ID REP2_YEAST
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                                                                                                                                                                                                                    EMBL; V01147; AAB59343.1; -.
EMBL; V01323; CAA24633.1; -.
PIR; A04504; PDBYC.
SGD; L0001512; REP2.
Plasmid; Trans-acting factor.
SEQUENCE 296 AA; 33196 MW;
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).

Plasmid 2-micron.

Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;

Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                              STRAIN-A364A D5;
                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL 1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TRANS-ACTING FACTOR C (REP2) (PROTEIN CHARLIE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
    \vdash
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   MDDIETAKNL
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                         Length: 296
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TVKARTAYSV WDVCRLFIEM IAPDVDIDIE SKRKSDELLF
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                           February 14, 2000 08:02 Type: P Check:
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                                                     E280A192 CRC32;
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!!AA_SEQUENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The identification of cryptic rhamnose biosynthesis genes in wisseria gonorrhoeae and their relationship to lipopolysaccharide biosynthesis.";

J. Bacteriol. 176:6915-6920(1994).

- i. CAPALYTIC ACTIVITY: DTDP-GLUCOSE = DTDP-4-DEHYDRO-6-DEOXY-D-1-COFACTOR: NAD.

- i. COFACTOR: NAD.

- i. PATHURAY. """.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE F
STRAIN=MS1
MEDIJIE: 94223693 ... CHERIF-ZAHAR B., SALVIGNOL I., BLANCHER A., MOURO I., LE VAN KIM C., CHERIF-ZAHAR B., SALVIGNOL I., BLANCHER A., CARTRON J.-P., COLIN Y.;

"Molecular characterization of the Rh-11ke locus and gene transcripts from the rhesus monkey (Macaca mulatta).";

"Mol. Evol. 38:169-176(1994).

"I- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.

"I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"I- SIMILARITY: BELONGS TO THE RH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (Rhesus macaque)
Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 028849;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
RH-LIKE PROTEIN (RHESUS-LIKE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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Lipopolysaccharide biosynthesis; Lyase; NAD.
Lipopolysaccharide biosynthesis; Lyase; NAD.
NP_BIND
13
19
NAD (POTENTIAL).
SEQUENCE 346 AA; 38828 MW; FB9FD6A3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z32742; CAA83652.1; -. EMBL; Z21508; CAA79718.1; -. PIR; S47045; S47045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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-i- SIMILARITY: STRONG, TO OTHER DTDP-GLUCOSE 4,6-DEHYDRATASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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[1]
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S47045; S
PFAM; PF01370;
                                                                                                                                                                                                                                                                                                                                                                                  Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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i; Cercopithecidae; Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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GLISIGGAKC

LPVCFNRVLG

351

VWASSNMIGF

QVLLSTGTLS

IHESHSVHYT LAMAMSITSG

LITGLLLNLK IWKGPHVAKY

FGLPALLGEI

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or send an email to license@isb-sib-
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TRANSMEM
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                                           151
                                                               101
251
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                      Erythrocyte;
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                                                                                                            ш
                     TTSPSLFAML
                                           TMRIVINNIF
                                                                                      QDLTVMAVLG
                                                                                                           SSKYPRSVRC CLPLWALTLE AALILLFFFF TYYDASLEDQ
 AISVSSLAHP
                                                                                                                                                                                                                                                                                                                                                                           S70343; AAB30637.1; PF00909; Ammonium_t
                                                                                                                               Length: 416
                                                                                                                                                      416 AA;
                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                             Ammonium_transp;
                                                                                      LGFFTSNLRR NSWSSVAFNL FLLALGVQWA
GGKINMTYMH
                                            KIDYGMNMMH
                                                                 SIRLATRSTM
                     GTLFLWMFWP
                                                                                                                                February 14, 2000 08:02 Type:
                                                                                                                                                      45672 MW;
NAALAGGVAL
                                            IHVFAAYFGL TVAWCLPKPL PKGTEDKYQT
                                                                 SMLISMNAVL
                      TENSALLLNP
                                                                                                                                                                                                                                                                                                                                                                                                          agreement (See http://www.isb-sib.ch/announce/@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 Polymorphism
                                                                                                                                                                  POTENTIAL.
POTENTIAL.
ROSING (IN
R -> K (IN
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P -> L (IN
G -> R (IN
Y -> C (IN
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7 -> C (IN
6AAE8F7F
                                                                 GKVNLVQLVV
 SASCHVIHSP
                        IERKNAVFST
                                                                                                                                                     MAC-B).
MAC-B).
MAC-B).
MAC-B).
MAC-B).
CRC32;
                                                                                                            KGLVASYQVC
 WIAMVLGLVA
                                                                  MELVELTVFG
                                                                                        ILLDGFLSQF
                                                                                                                                  ש
                                                                                                                                  Check:
                                                                                                                                    4371
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RHO7, HUMAN STANDARD, PRT; 227 AA. 552138; 099535; 000690; 000734; 01-007-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last anotation update) RHO-RELATED GTP-BINDING PROTEIN RHO7.
                                                                                                                                                                                                      SEQUENCE 1.0
                                                                                                                                                                                                                                      401
SEQUENCE FROM N.A.
MEDLINE; 97092865.
SMITH T.M., LEE M.K.,
HOOD L., KING M.-C.;
                                                                                                        Eutheria; Primates;
                                                                                                               RHO7.
Homo sapiens (Human).
---- Metazoa; Chordata;
                                                     Submitted
                                                                                   EQUENCE FROM N.A.
                                                                         ISSUE-BRAIN;
                                                                                                                                                                                                                                      FDDQAFWEFP
                                                     (FEB-1996)
                                                                                                                                                                                                                                     HLAVGE
                                                                                                          Chordata; Craniata; Ve. Catarrhini; Hominidae;
                                                     ö
            SZABO
                                                     the
            C.I.,
                                                     EMBL/GenBank/DDBJ
            JEROME N.,
                                                                                                                     Vertebrata;
            MCEUEN M., TAYLOR M.,
                                                     databases
                                                                                                                     Mammalia;
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IIAA_SEQUENCE 1.0

ID RIB7_ARCFU
AC 022872;
DT 15-DEC-1999 ()
DE 7021 ()
DE 702
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GTP-binding; Prenylation; I
NP_BIND 14 21
NP_BIND 61 65
NP_BIND 119 122
DOMAIN 36 44
                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390;364-370(1997).
-!- CATALYTIC ACTIVITY: 5-AMINO-6-(5-PHOSPHORIBITYLAMINO)URACIL + NADP(+) = 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL + NADP(+) = 5-AMINO-6-(5-PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANT-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P. CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.F.

RICHARDSON D.L., KERLANGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GIIL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENLY K., ADAMS M.D., LOFTUS B. PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHO OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T. COTTON M.D., SPRIGGS T., ARTIACH P., KANNE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., D'ANDREA K.P., BOWMAN C., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PUTATIVE 5-AMINO-6-(5-PHOSPHORIBOSYLAMINO)URACIL
(EC 1.1.1.193) (HTP REDUCTASE)
AF2007.
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EMBL; L78833; AAC37595.1;
HSSP; P06749; 1A2B.
MIM; 601555; -.
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-!- SIMILARITY: BELONGS TO THE RHO FAMILY IN THE RAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

EFFECTOR REGION (POTENTIAL).

GERANYL-GERANYL (BY SIMILARITY).

MW; 9B964266 CRC32;
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SYKES S.M.,
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RIPA_LUFCY Length: 277

February 14, 2000 08:02

Type:

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Check:

429

ACT_SITE SEQUENCE

179 277

179 30212 MW;

ВХ

E0233100 CR

CRC32;

AA;

SIGNAL CHAIN

20

PROSITE; PS00275; SHIGA_RICIN; PFAM; PF00161; RIP; 1. Antiviral; Protein synthesis in

synthesis inhibitor; Hydrolase; 19 277

Toxin; Signal. PROTEIN LUFFIN-

ISSP;

P16094;

1AHB

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RIB7_ARCFU Length: 219
                                                                                                                                                                                                                                                                                                                             MEDILINE; 92288316.

KATAOKA J. HABUKA N., MIYANO M., MASUTA C., KOIWAI A.;

"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
inactivating protein from Luffa cylindrica.";

Plant Mol. 18:1199-1202(1992).

-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT O
SPECIFIC ADENOSINE ON THE 28S RNA.

-i- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
PROTEINS. BELONGS TO TYPE 1 RIP.

PROTEINS. BELONGS TO TYPE 1 RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000465;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
RIBOSOME-INACTIVATING PROTEIN LUFFIN-ALPHA PRECURSOR
N-GLYCOSIDASE) (EC 3.2.2.22)
N-GLYCOSIDASE) (EC 3.2.2.22)
                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                         EMBL; X62371; CAA44229.1;
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Luffa cylindrica (Smooth Loofah) (Sponge gourd).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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MKRETVLILA IFVAASTVEA DVRESLSGSS STSYSKFIGD LRKALPSNGI

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SOUTH THE PROPERTY OF THE PROP
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protein from sponge gourd (Luffa cylindrica) see
Agric Biol Chem. 55:229-238(1991).

- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-
SPECIFIC ADENOSINE ON THE 28S RNA.

-! SIMILARITY: TO OTHER BACTERIAL AND PLANTS RI-
PROTEINS: BELONGS TO TYPE 1 RIP.

1 NO108: JN0108.

HSSP: P16094; 1MOM.

PROSITE: P5900275; SHIGA_RICIN; 1.
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01-MAR-1992 (
01-OCT-1996 (
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TISSUE-SEED;
MEDLINE; 912;
  SEQUENCE;
                                                                                                                                                                                                                                                                                                  SEQUENCE 1.0
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytas; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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01-AUG-1991 (Rel. 19,
15-JUL-1999 (Rel. 38,
RIBOSOME-INACTIVATING
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                                                              Spinacia.
                                                                          Spinacia oleracea (Spinach)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae;
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ACT.SITE 160 160 BY SIMILARITY
SEQUENCE 250 AA; 27293 MW; 64A72993 CRC32;
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PROTEIN LUFFIN-B (RRNA
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                      56-67
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r PRECURSOR
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seeds.";
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!!AA_SEQUENCE 1.0
ID RR8_MARPO
AC P06362;
DT 01-JAN-1988 (
DT 01-JAN-1988 (
DT 01-FEB-1996 (
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"Structure and expression of the nuclear gene coding for the chloroplast ribosomal protein L21 developmental regulation of a housekeeping gene by alternative promoters.";

MO1. Cell. Biol. 13:2614-2622(1993).

-i- FUNCTION: THIS EROTEIN BINDS TO 23S RIBOSOMAL RNA IN THE PRESENCE OF PROTEIN L20 (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE L21P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X56691; CAA40019.1; -.
EMBL; M574113; AAA34041.1; -.
EMBL; M64682; AAA74715.1; -.
PIR; S13527; S13527.
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STRAIN-CV. GEANT D'HIVER;
MEDLINE; 93205007.
LAGRANGE T., FRANZETTI B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90375547.

SMOOKER P.M., KRUFT V., SUBRAMANIAN A.R.;

"A ribosomal protein is encoded in the chloroplast

"A ribosomal protein is encoded in the chloroplast

plant but in the nucleus in angiosperms. Isolation

protein and cDNA clone with transit and an unusual

13. Biol. Chem. 265:16699-16703(1990).
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"Hypothesis for the evolutiona
protein L21 of spinach.";
Curr. Genet. 18:553-556(1990).
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                                                                                                    CHLOROPLAST
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18 (Rel. 06, Last sequ
16 (Rel. 33, Last anno
17 30S RIBOSOMAL PROTE
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                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56-75
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spinach L
sequence.
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Marchantia polymorpha (Liverwort) Chloroplast. Eukaryota; Viridiplantae; Strepto

Viridiplantae;

Streptophyta;

Embryophyta;

Marchantiopsida;

SO WERE REPORTED TO THE PROPERTY OF THE PROPER

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RR8_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1.0
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                     GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V. submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
                                                                    STRAIN-972;
GENTLES S.,
                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
40s RIBOSOMAL PROTEIN S13.
RPS13 OR SPAC6F6.07C.
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PIR; A02716; R3LV8.
HSSP, P56209; ISBI.
MENDEL; 13155; MARPO; TPS8; 1.
PROSTITE; P5000053; RIBOSOMAL_S8; 1.
PFAM; PF00410; Ribosomal_S8; 1.
RIbosomal protein; TRNA-binding; Chloroplast.
RIbosomal protein; TRNA-binding; Chloroplast.
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 92375702.
MARKS J., SIMANIS V.;
"Cloning of the gene for ribosomal protein Schizosaccharomyces pombe.";
Nucleic Acids Res. 20:4094-4094(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 322:572-574 (1986).
Nature 322:572-574 (1986).
-I- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
-I- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMESONO K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUKUZAWA H., KOHCHI T., OZEKI H., OHYAMA K.;
                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OZEKI
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 This SWISS-PROT
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[1]
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Mol. Biol. 203:333-351(1988).
                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorpha chloroplast DNA.";
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CHANG Z.,
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is produced
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INIT_MET 0
SEQUENCE 150 AA;
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                                                                                                      AVSHVEIERL KELKVKKRVK ITLHSGKPGV
                                                                                                                                       MGQKVNPIGF
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KWYADKKIVP

KFLNKKYNNA ETIASLEKLI

VIGREAATMK ALVKEDAVIR

NHGGGKRRPS

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MEDLINE; 94169035.

TOTH K.T., HARRISON N., SEARS B.B.;

TOH SEARCH CONTROL OF THE SEARCH OF THE BINDING OF INITIATORY

METTRNA (BY SIMILARITY).

1. SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
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EMBL; Z98981; CAB11741.1; --
PIR; Z98981; CAB204; CAB204;
                                                                                                                                                                                                                                                                  EMBL; L22465; AAA21916.1; PROSITE; PS00548; RIBOSOM
                                                                                  PROSITE; PS00548; RIBOSOMAL_S3; 1.
PFAM; PF00189; Ribosomal_S3_C; 1.
PFAM; PF00417; Ribosomal_S3_N; 1.
Ribosomal protein; tRNA-binding.
SEQUENCE · 257 AA; 28717 MW; 803552CF CRC32;
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01-FEB-1995 (Rel. 31, Last sequence up
01-FEB-1995 (Rel. 31, Last annotation
30s RIBOSOMAL PROTEIN S3.
RPSC OR RPS3.
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     February 14,
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16822 MW;
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Acholeplasma.
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C75B8E0E CRC32;
2000 08:02 Type:
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AA_SEQUENCE 1.0

D RSB_SYNY3 STANDARU,
AC P73307;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence updat
DT 01-NOV-1997 (Rel. 35, Last annotation up
TO RIBOSOMAL PROTEIN SB.
TOR RIBOSOMAL PROTEIN SB.
TOR STANDARD PCC 6803).
                                   CCCCCRTT RAX RANCOSOS
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SEQUENCE FROM N.A.

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SEQUENCE: 96196179.

MEDIINE; 96196179.

TONG J., WETMUR J.G.;

TONG J., WETMUR J.G.;

"CLONING; sequencing, and expression of ruvB and characterization of "CLONING; sequencing, and expression of the ruvB proteins from two distantly related thermophilic eubacteria.";

J. Bacteriol. 178:2695-2700(1996).

IBacteriol. 178:2695-2700(1996).

ICRUCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES CRUCTIONS IN THE RUVAL RUVAL WITH PALINDROMIC SEQUENCE, INDICATING THAT I MAY PROMOTE STRAND EXCHANGE REACTIONS IN INDICATING THAT MEDIATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROSAWA M., SUGJURA M., SASAMOTO S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
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HSSP; P56209; ISEI.
PROSITE; P$00053; RIBOSOMAL_S8; 1.
PFAM; PF00410; RIBOSOMAL_S8; 1.
PFAM; PF00410; RIBOSOMAL_S8; 1.
14666 MW; 3596E999 CRC32;
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                                                                                                                                                                                                                      Thermus aquaticus (subsp. the
Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
11-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
10LLIDAY JUNCTION DNA HELICASE RUVB.
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Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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RUVB_THETH
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SMILLIE D.A TTTT
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BLATTMER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
GREGOR J., DAVIS N.W., KI
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1.0

STANDARD; PRT: 217 AA.

P26428; P76673;

01-AUG-1992 (Rel. 23, Created)
01-NOV-1995 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
SIGMA CROSS-REACTING PROTEIN 27A (SCRP-27A).
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-!- SUBUNIT: FORMS A COMPLEX WITH RUVA.
-!- SIMILARITY: TO OTHER ATP-BINDING DNA REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA repair; SOS response; ATP-binding; DNA recombination; NP_BIND .45 52 ATP (POTENTIAL). SEQUENCE 324 AA; 36015 MW; D9638BD3 CRC32;
                                                             Biochem.
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Submitted (XXX-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria;
  : :
                                                                                                                        SEQUENCE OF 1-24.
MEDLINE, 92246944.
UESHIMA R., FUJITA N., ISHIHAMA A.;
"Identification of Escherichia coli
antibodies against region 2.2 peption of the colimate of the coli
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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            chem. Biophys. Res. Cc
FUNCTION: NOT KNOWN.
2.2 OF RPOD AND RPOH.
SIMILARITY: BELONGS T
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nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                          G. III, BLOCH C.A., PERNA N.T., J., GLASNER F.D., RODE C.K., MA KIRKPATRICK H.A., GOEDEN M.A., R
                                                                                    Commun
                    TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOWNSLEY F.M., ISHIHAMA A., HAYWARD the EMBL/GenBank/DDBJ databases.
                                                             Ommun. 184:634-639(1992)
CROSS-REACTS WITH ANTIB
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polymerase sigma
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, MAYHEW G.F.,
., ROSE D.J.,
                                                               AGAINST REGION
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A SICHERITZ-PONTEN T., ALSWARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,

A ERIKSSON A.S., WINLER H.H., KURLAND C.G.;

IT The genome sequence of Rickettsia prowazekii and the origin of

IT mitochondria.";

A mature 396:133-140(1998).

C -! FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE

TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE,

C -! FUNCTION THE TRANSLOCATION OF PROTEINS (SECA-F & SECY) THAT

C COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS (BY

SUBCLILULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

C -! SUBLILARITY). GECOATION: INTEGRAL MEMBRANE PROTEIN.

C -! SUBLILARITY: BELONGS TO THE SECY/SECG1-ALPHA FAMILY.
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                        EMBL; AJ235272; CAA15079.1;
PROSITE; PS00755; SECY_1; F
PROSITE; PS00756; SECY_2; I
Protein transport; Transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PREPROTEIN TRANSLOCASE SECY SUBUNIT.
SECY OR RE639.
Rickettsia prowazekii.
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ANDERSSON S.G.E.,
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EMBL; U18997; AAA58011.1; ALT_INIT.
EMBL, AE000400, AAC76241.1; ALT_INIT.
PIR; JN0287; JN0287.
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STRAIN=MADRID E;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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195 217
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AQNIAEAASGIDKLVSRVLVLAE
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transport;

SECY_1; FALSE_NEG.
SECY_2; 1.
Transmembrane; Translocation; 77ansmembrane; Translocation

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ALD DEFINE REPORT OF THE PROPERTY OF THE PROPE
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-I-FUNCTION: EMHIBITS PHOSPHOHISTIDINE PHOSPHATASE ACTIVITY TOWARDS --I-FUNCTION: EMHIBITS PHOSPHOTASE ACTIVITY TOWARDS THE HPT DOMAIN OF THE ARCB SENSOR INVOLVED IN THE MULTISTEP HIS-
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STRAIN-K12 / MC4100;
MEDIINE; 98149313.
MEDIINE; 98149313.
An Escherichia coli protein that exhibits phosphohistidine phosphatase activity towards the HPt domain of the ArcB sens involved in the multistep His-Asp phosphorelay.";
Mol. Microbiol. 27:573-583(1998).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 9742661]
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T.
BLATTNER F.R., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MERIEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MERIEGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,
MRU B., SHAO Y.;
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat)
PHOSPHOHISTIDINE PHOSPHATASE SIXA (EC 3.1.3
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                   Escherichia coli K-12.";
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3.1.3.-) (RX6).
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AQETFHQVNQ AEVMANSDKA

MNIFIMRHGE

RHLTVYGSKQ AFLQGQWLKQ

EIWEGITPYG

HAHSVIDYLE HLSTLVINSL

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SIXA_ECOLI Length: 161
 SIXA_HAEIN
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 36, Last sequence
15-JUL-1998 (Rel. 36, Last annotatic
PHOSPHOHISTIDINE PHOSPHATASE SIXA HC
SIXA OR HI1338.
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                                                                                                                                                                                                                                                                  FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FIIZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDDELOM E., COTTON M.D., UTTERBACK T.R., PHILLIPS C.A., SPRIGGS T., HEDDELOM E., COTTON M.D., ETINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
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EMBL; D800322; AAC75400.1;
EMBL; D90864; CAB22123.1; --
EMBL; D90865; CAB22129.1; --
ECOGENE; EG14126; SIXA.
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as incompanies.
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Bacteria; Proteobacteria;
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                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                   EMBL; U32813; AAC22985.1; TIGR; HI1338; -.
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161 AA;
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Virulence.

159

166

transport; ATP synthesis;

STYGENE; SG10464; SPAL.
PROSITE; PS00152; ATPASE_ALPHA_BETA;
PFAM; PF00006; ATP-synt_ab; 1
Hydrolase; Hydrogen ion transport; Al

EMBL; U08279; AAA74038.1; EMBL; X73525; CAA51921.1; EMBL; U10872; AAA83429.1; PIR; S37304; S37304.

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SPAL_SALT
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MEDILINE; 9527391.

MEDILINE; 9527391.

MEDILINE; 9527391.

Functional analysis of the Salmonella typhimurium invasion genes invl and invJ and identification of a target of the protein secretion apparatus encoded in the inv locus.";

MO1. Microbiol. 15:25-38(1995).

-i- FUNCTION: NECESSARY FOR EFFICIENT ENTRY OF S.TYPHIMURIUM INTO CULTURED EPITHELIAL CELLS. PROBABLE CATALYTIC SUBUNIT OF A PROTEIN TRANSLOCASE. MAY ENERGIZE THE PROTEIN EXPORT APPARATUS ENCODED IN THE INV LOCUS WHICH IS REQUIRED FOR THE SUBFACE PRESENTATION OF DETERMINATS NEEDED FOR THE ENTRY OF SALMONELLA SPECIES INTO
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STRAIN=SRI1 / SL1344;
STRAIN=SRI1 / SL1344;
MEDLINE; 94321319.
EICHELBERG K., GINOCCHIO C.C., GALAN J.E.;
"MOLECULar and functional characterization
"Molecular and functional characterization
typhimurium invasion genes invB and invC: h
FOF1 ATPase family of proteins.";
J. Bacteriol. 176:4501-4510(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROISMAN E.A., OCHMAN H.;
"Cognate gene clusters govern
Salmonella typhimurium and Shi
EMBO J. 12:3779-3787(1993).
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Bacteria; Proteobacteria;
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PROBABLE AIP SYNTHASE SPAL/INV
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STRAIN=SR11 / SL1344
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SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
SIMILARITY: TO OTHER TRANSPORT APPARATUS ATPASES
BETA SUBUNIT.
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Shigella flexneri.";
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                                                                                                                                                                                                                                                                                       MEDLINE; 91008990.

CHEVALIER C., SAILLARD C., BOVE J.M.;

"Spiralins of Spiroplasma citri and Spiroplasma melliferum: amino acid sequences and putative organization in the cell membrane.";

J. Bacteriol. 172:6090-6097(1990).

-i- SUBJURT: SEBUS TO OCCUR AS DIMER, TETRAMERS, AND LARGE OLIGOMERS OF IDENTICAL CHAINS.
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CONFLICT
CONFLICT
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Bacteria, Firmicutes, Bacillus/Clostridium group; Mollicutes;
Spiroplasmataceae; Spiroplasma.
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01-MAY-1991 (Rel.
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    SEQUENCE
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STRAIN-ATCC 33219 / BC3;
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                            DOMAIN
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POTENTIAL.
CYTOPLASMIC.
CYTOPLASMIC (POTENTIAL).
PALMITATE (POTENTIAL).
W; 286BDF9D CRC32;
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G -> A (IN REF. 2).

CAKISITIGRCRCG -> GENIDNDRAMOMR (IN REF. 2).

R -> W (IN REF. 2).
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SPIR_SPIME

Length: 241

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February 14, 2000 08:02

Type: P Check:

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It is

produced through a collaboration

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                   SEQUENCE FROM N.A.

STRAIN-IT2:

MEDLINE; 97885756.

MEDLINE; 97885756.

KUBO T., HOLDEN D.W.;

"Functional analysis of ssaJ and the ssaK/U operon, 13 genes encocomponents of the type III secretion apparatus of Salmonella Pathogenity Island 2.";

Pathogenity Island 2.";

Pathogenity Island 2.";

Pathogenity Faland 2.";

PATHOGENITY SART OF A TYPE III SECRETION SYSTEM.

-1. FUNCTION: PART OF A TYPE III SECRETION SYSTEM.

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-1. SIMILARITY: BELONGS TO THE FLHB/HRPN/YSCU/SPAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seg
15-DEC-1999 (Rel. 39, Last ann
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MEDLINE; 91267949.

EVERETT K.D.E., HATCH T.P.;
EVERETT K.D.E. and lipid modification of the cysteine-rich envelope proteins of Chlamydia psittaci 6BC.";

J. Bacteriol. 173:3821-3830(1991).
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Bacteria; Chlamydiales;
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01-OCT-1996 (Rel. 34, Last
01-OCT-1996 (Rel. 34, Last
SULFUR-RICH PROTEIN.
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AC P30872;
AC P30872;
DT 01-JUL-19;
DT 01-FBB-19;
DT 01-FBB
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   mouse Somatostatin receptors expressed in brain, gastrointestinal tract, and kidney.",

Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

PROC. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

PUNCTION: RECEPTOR FOR SONATOSTATIN WITH HIGHER AFFINITY FOR SONATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED VIA PERTUSSI TOXIN SENSITIVE G PROTEINS TO INHIBITION OF ADENTAL CYCLASE. I ADDITION IT STIMULATES PHOSPHOTROSINE PHOSPHATASE AND NA+/H-EXCHANGER VIA PERTUSSIS TOXIN INSENSITIVE G PROTEINS.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

TISSUE SPECIFICITY: ETTAL KIDNEY, FETAL LIVER, AND ADULT PANCRE BRAIN, LUNG, JEJUNUM, AND STOMACH.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Y. POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

YOunding and functional characterization of a family of human and

"Cloning and functional characterization of a family of human and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-FEB-1996 (Rel.
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tein transport; Transmembrane.
4 54 POTENTIAL.
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!!AA_SEQUENCE
ID SSR1_MOUS
AC P30873;
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GCRDB; GCR_02
MIM; 182451;
PROSITE; PSOC
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01-JUL-1993 (Rel. 26, L
01-NOV-1997 (Rel. 35, L
SOMATOSTATIN RECEPTOR T
SSTR1 OR SMSTR1.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 92108031.

YAMADA Y., POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

YAMADA Y., POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

YAMADA Y., POST S.R., WANG K., TAGER H.S., BELL G.I., SEINO S.;

"Cloning and functional characterization of a family of human and mouse somatostatin receptors expressed in brain, gastrointestinal tract, and kidney.";

Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).

PROC. NATL. Acad. Sci. U.S.A. 89:251-255(1992).

PROC. NATL. Acad. Sci. U.S.A. 89:251-255(1992).

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detazoa; Chordata; Craniata; Vertebrata;
dentia; Sciurognathi; Muridae; Murinae;
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PALMITATE (POTENTIAL).
28C01B27 CRC32;
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SSR1_MOUSE
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TRANSMEM
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DOMAIN
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PIR; C41795; (
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                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-EBB-1996 (Rel. 33, Last annotation update)
SOMATOSTATIN RECEPTOR TYPE 1 (SSIR) (SRIF-2).
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                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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MEDLINE;
         SEQUENCE FROM N.A. STRAIN-WISTAR; TI
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92096119
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           TISSUE-BRAIN
                                                                                                                                                        STANDARD;
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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POTENTIAL.

BY SIMILARITY.

BY SIMITATE (POTENTIAL).

PALMITATE (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                Mammalia;
Rattus.
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ISFIXSVVCL VPFLVTSTLL

CGEGVCSRGP VGLCGNSMVI RHWPFGALLC

MFPNGTAPSP TSSPSSSPGG

GSGAADGMEE PGRNSSQNGT

NSDGTVACNM LMPEPAQRWL

VGFVLYTFLM

GFLLPVGAIC LCYVLIIAKM

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YVILRYAKMK RLVLSVDAVN VWVLSLLVIL

TATNIYILNI METSIYCLTV PIVVESRTAP

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SSR1_RAT
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GCRDB; GCR_0628; --
PROSITE; PS00237; G_F
PFAM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                           G-protein
Multigene
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LI X. -J., FORTE M., NORTH R.A., ROSS C.A., SNYDER S.H.;

"Cloning and expression of a rat somatostatin receptor enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEYERHOF W., PAUST H.J., SCHOENROCK C., RICHTER D.;
"Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed in specific rat brain regions.";
DNA Cell Biol. 10:689-694(1991).
                                                 CARBOHYD
CARBOHYD
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DISULFID
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-!- FUNCTION: RECEPTOR FOR SOMATOSTATIN WITH HIGHER AFFINITY FOR SOMATOSTATIN-14 THAN -28. THIS RECEPTOR IS COUPLED TO PHOSPHOTYROSINE PHOSPHATASE AND NA+/H+ EXCHANGER VIA PERTUSSIS TOXIN INSENSITYEE G PROTEINS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: BRAIN, PITUITARY, ISLET, JEJUNUM, STOMACH, HEART, SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brain.";
J. Biol. Chem.
-!- FUNCTION: I
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DOMAIN
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PIR; A45102; A45102
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                          SEQUENCE
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                                                                                                                                                                                                                                                                    RANSMEM
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Length: 391
                                                                                                                                                                                                                                                                                             0001; 7tm_1; 1.
coupled receptor;
family; Lipoprote
                           Ą,
                                              February
                                                                                                                                                                                                                                                                                                                                                                                              NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                               PROTEIN_RECEPTOR; 1.
                           42746 MW;
  14, 2000 08:02 Type: P Check: 9240
                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
POTENTIAL.
POTENTIAL.
BY SIMILARITY.
BY SIMILARITY (POTENTIAL).
PALMITATE (POTENTIAL).
W; 8AFE45D5 CRC32;
                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein;
                                                                                                                                                                              4 (POTENTIAL).
EXTRACELLULAR
                                                                                                                                                                                                       3 (POTENTIAL)
CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                        CYTOPLASMIC
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SSRB_CANFA
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MEDLINE;
GOERLICH
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WADA I., RINDRESS D., CAMERON P.H., OU W.-J., DOHERTY J.J. II,
LOUVARD D., BELL A.W., DIGNARD D., THOMAS D.Y., BERGERON J.J.M.;
"SSR alpha and associated calnexin are major calcium binding proteins
of the endoplasmic reticulum membrane.";
of the endoplasmic reticulum membrane.";
1. Blol. Chem. 266:19599-19610(1991).
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                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it uses by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used by non-profit institutions as long as its content is in no was used to be a superior of the content in the long as its content is in no was used to be a superior of the long as its content is in no was used to be a superior of the long as its content is in no was used to be a superior of the long as its content is in no was used to be a superior of the long as its content is in no was used to be a superior of the long as its content is in no was used to be a superior of the long as its content is in the long as its content is 
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 18-42; MEDLINE; 92011761.
                                                                                                                                DOMAIN
                                                                                                                                                                                       GIYCOPTOTEIN;
SIGNAL
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Cell Biol. 111:2283-2294(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF ER RESIDENT SUBUNIT: HETEROTRAP-GAMMA.
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B37273; B37273
S15510; S15510
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170
170
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104
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HETEROTETRAMER OF TRAP-ALPHA,
                                                                                                                                                                                           Signal;
  183
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. 34, Last annotation update)
rATED PROTEIN, BETA SUBUNIT PRECURSOR
RECEPTOR BETA SUBUNIT) (SSR-BETA) (GE
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169
183
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  February
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CYTOPLASMIC (POTENTIAL)
POTENTIAL.
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                                       977848EB CRC32;
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Type:
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(GP25H).
    ש
                                                                                                                                                                        PROTEIN,
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    Check:
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      8392
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101 GYENFTSATV TYLAQEDGPV VIGFTSAPGQ GGILAQREFD RRFSPHFLDW
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151 AAFGYMTLPS IGIPLLLWYS SKRKYDTPKS KKN

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"Cloning and sequence analysis of the beta s ranslocon-associated protein.";
Biochim. Biophys. Acta 1217:101-102(1994).
-i. FUNCTION: TRAP PROTEINS ARE PART OF A COBIND CA(2+) TO THE ER MEMBRANE AND THERE OF ER RESIDENT PROTEINS.
-i. SUBUNT: HETEROTETRAMER OF TRAP-GAMMA.
TRAP-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _SEQUENCE 1.0
SSRB_HUMAN
  DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement in not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

01-OCT-1996 (Rel. 34, Last annotation updat

TRANSLOCON-ASSOCIATED PROTEIN, BETA SUBUNIT
                                                                                                                                                                                                                   EMBL;
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SSR2.
Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; Cr.
'`rates; Catarrhini;
                                                                                                                                          CHAIN
                                                                                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                   MIM; 600867
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                                                                                                                                                                                                                                                                                                                                                                                                                      RETICULUM.
                                                                                                                                                                                                                     X74104; CAA52207.1;
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104
183 AA;
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150
170
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                                                                                                                                                            Signal; Endoplasmic reticulum; Transmembrane
1 17 BY SIMILARITY.
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                                                                                                                                          183
    20135 MW;
                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
POTENTIAL.
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                                                                                                                        SUBUNIT
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                                                                                                      LUMENAL
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      B2E82B37 CRC32;
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                                                                                                    (POTENTIAL).
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EREBY REGULATE
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                                                                                                                                            PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
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SSRB_HUMAN Length: 183 February 14, 2000 08:02 Type: P Check: 8093

- 1 MRLLSFVVLA LFAVTQAEEG ARLLASKSLL NRYAVEGRDL TLQYNIYNVG
- 51 SSAALDVELS DDSFPPEDFG IVSGMLNVKW DRIAPASNVS HTVVLRPLKA
- 101 GYFNFTSATI TYLAQEDGPV VIGSTSAPGQ GGILAQREFD RRFSPH
- 151 AAFGYMTLPS IGIPLLLWYS SKRKYDTPKT KKN

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IIAA_SEQUENCE 1.0
IID ST14_SOLTU STANDARD; PRT; 214 AA.
AC 041495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE STS14 PROTEIN PRECURSOR.
GN STS14.
OS Solanum tuberosum (Potato).
OS Solanum tuberosum (Potato).
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1 51

IVSGMLNVKW DRIAPASNVS HTVVLRPLKA

MRLLASVLLA LFAVSHAEEG
SSAALDVELS DDSFPPEDFG

ARLLASKSLL

NRYAVEGRDL TLQYNIYNVG

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ST14_SOLTU
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"MOISCULIAR analysis of a pistil-specific gene ex and cortex of Solanum tuberosum.";

plant Moi. Biol. 30:171-176(1996).

-!- FUNCTION: MAY PROTECT THE OUTER TISSUES OF T PATHOGEN ATTACK.

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE CORTEX THROUGHOUT PISTIL DEVELOPMENT. NOT EX ORGANS.
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SIGNAL 1
CHAIN 20
REPEAT 13
DOMAIN 59
SEQUENCE FROM N.A.
STRAIN-RD / KW20;
MEDLINE; 95350630;
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M.,
KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
                                                                                                                                                        P44847;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
SUFI PROTEIN HOMOLOG PRECURSOR.
SUFI OR HI0733.
                                                                                                                                                                                                                                                                 SEQUENCE 1.0
                                                                                                                              Haemophilus
Bacteria; P:
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HSSP; P04284; ICFE.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; FALSE_NEG
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; FALSE_NEG
PFAM; PF00188; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               Haemophilus
                                                                                                                                                                                                                                                   SUFI_HAEIN
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core eudicots;
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SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                            AEKKFYNYEN
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEVLSTAMAC
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                                                                                                                             us influenzae.
Proteobacteria;
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                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                             gamma subdivision; Pasteurellaceae;
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STS14 PROTEIN.
3.5 X 2 AA TANDEM REPEAT
POLY-PRO.
, 06BC0717 CRC32;
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OTHER
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IIAA_SEQUENCE 1.0
ID SUH3_RAT
AC P50235;
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(STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;

(STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OGURA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OKUDA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OKUDA K., SATSUKAWA M., OKUDA H., HIRATSUKA A.;

(MATABE T., OKUDA H., HIRATSUKA A.;

(MATABE T., OKUDA M., OKUDA H., HIRATSUKA A.;

(MATABE T., HIRATSUKA A.;

(MATABE T., HIRATSUKA A.;

(MATABE T., HIRATSUK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID
SULFOTRANSFERASE) (ST)
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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SCIENCE 269:496-512(1995).

SCIENCE 269:496-512(1995).

-!- SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).

-!- SUBCELLULAR STRONG, TO E.COLI AND S.TYPHIMURIUM SUFI.

-!- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.

-!- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
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68
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311
164
184
34496
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SUFI PROTEIN HOMOLOG
PLASTOCYANIN-LIKE.
; 8065147D CRC32;
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                                GROWTH HORMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
Rattus.
                                                                                                                                                                                   AND XENOBIOTICS
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I R.C.,
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HORMONE

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SUH3_RAT
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                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and applications of the two/three-base endonuclease R.CviII from II-3A virus-infected CGene 157:37-41(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
TYPE II RESTRICTION ENZYME CVIJI (EC 3.1.21.4) (ENDONUCLEASE CVIJI)
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D14989; BAA03634.1; - PFAM; PF00685; Sulfotransfe
                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKOWRON P.M., SWAMINATHAN N., MCMASTER K.,
                EMBL; U09001; AAC55064.1; -. REBASE; RB00873; CviJI.
                                                                                                                                                                            NOT YGCR.
-!- COFACTOR: REQUIRES MAGNESIUM.
                                                                                                                                                                                                                     "MOlecular cloning of the three base restriction endonuclease R.CviJII from enkaryotic Chiorella virus II-3A.";
Nucleic Acids Res. 24:2463-2469(1996).
The capalytic Activity: Reconizes The Presence of ATP, THERE IS A RELAXATION OF ITS SPECIFICITY AND IT CAN CLEAVE RETO. AND YECY, BUT
                                                                                                                                                                                                                                                                                                                                  SWAMINATHAN N., MEAD D.A., MCMASTER K., GEORGE D., VAN ETTEN J.L.,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE; 96292246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEAD D.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                   P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus IL-3A (CV-IL3A).
dsDNA viruses, no RNA stage; Phycodnaviridae;
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 Nuclease;
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 Restriction
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system; Magnesium
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                                                                                                       EMBL; X59869; CAA42526.1; -.
EMBL; X59870; CAA42527.1; -.
EMBL; X59871; CAA42528.1; -.
EMBL; X63901; CAB56795.1; -.
PIR; S16645; S16645.
PIR; A38095; A38095.
TRANSFAC; T00999; -.
TRANSFAC; T01001; -.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)
(TRANSCRIPTION FACTOR-7).
TCF7 OR TCF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDITINE; 92235082.

VAN DE WETERRING M.L., OOSTERWEGEL M.A., HOLSTEGE F., DOOYES D.,

VAN DE WETERRING M.L., OOSTERWEGEL M.A., CLEVERS H.:

SUJJKERBUIJK R., GEURTS VAN KESSEL A., CLEVERS H.:

"The human T cell transcription factor-1 gene. Structure,

"The human T cell transcription factor-1 gene. Structure,

localization, and promoter characterization.";

J. BJOL. Chem. 267:8330-8536(1992).

J. BJOL. Chem. 267:8330-8536(1992).

J. FURCTION: TRANSCRIPTIONAL ACTIVATOR INVOLVED IN T-CELL LYMPHOCYTE

DIFFERENTIATION. IT BINDS TO THE T-LYMPHOCYTE-SPECLIFIC ENHANCER

ELEMENT (5-WWCAAAG-'3') FOUND IN THE PROMOTER OF THE CD3-EPSILON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P36402;
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Homo sapiens (Human).
Eukaryota; Metazoa; C
Eutheria; Primates; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAN DE WETERING M.I., OOSTERWEGEL M.A., DOOIJES D., CLEVERS H.; "Identification and cloning of TCF-1, a T lymphocyte-specific transcription factor containing a sequence-specific HMG box.", EMBO J. 10:123-132(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: THREE DIFFERENT FORMS THAT DIFFER IN THE C-TERMINAL SECTION ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: T-CELL SPECIFIC.
SIMILARITY: CONTAINS 1 HMG BOX.
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                             Nuclear protein;
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                             Transcription regulation; Activator;
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
EMBL; AJ000491; CAA04129.1; -. EMBL; AJ010063; CAA08987.1; -. EMBL; AJ011098; CAA09479.1; -.
                                                                                                                                                                                                                                                                                    MUES A., GAUTEL M.;
"Structure of the human
Submitted (SEP-1998) to
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PALLAVICINI A., VALLE G., LANFRANCHI G.;
"Human telethonin genomic sequence.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created).
15-JUL-1998 (Rel. 36, Last sequence update).
15-JUL-1999 (Rel. 39, Last annotation update).
15-JUC-1999 (Rel. 39, Last annotation update).
TELETHONIN (TITIN CAP PROTEIN).
THOMO Sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VARSPLIC
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                                                                                                                                                                                                                                     INTERACTION WITH TITIN.
MEDLINE: 98307394.
MUES A., VAN DER VEN P.F.,
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WALLE G., FAULKNER G., DE ANTONI A., PACCHIONI B., PALLAVICINI PANDOLFO D., TISO N., TOPPO S., TREVISAN S., LANFRANCHI G.; Telethonin, a novel sarcomeric protein of heart and skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLINE; 98010471.
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                                                                                                                                                                                                                                                                                 telethonin gene.";
the EMBL/GenBank/DDBJ databases
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ETHMPRELKDGNGQESLSMSSSSSPA -> GGKRNAFGTYP

EKRAAPAPAPFLPMTVL (IN ISOFORM B).

ETHMPRELKDGNGQESLSMSSSSSPA -> DPGSPKKCRAR

FGLNQQTBMCGPCR (IN ISOFORM C).

7BB387D9 CRC32;
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OCCUPATION NO OC
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ID TRAM_AGRT6
AC Q57471;
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15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
TELETHONIN (ITIN CAP PROTEIN).
Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia: Eukaryota: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
TRANSCRIPTIONAL REPRESSOR TRAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases I- FUNCTION: MUSCLE ASSEMBLY REGULATING FACTOR.
I- SUBCELLULAR LOCATION: SARCOMERIC.
I- SUBUNIT: INTERACTS WITH TITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SEQUENCE 1.0
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"The titin cap protein formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVOLETLA C., FORMENTIN E., VALLE G., LANFRANCHI G.; Skeletal_muscle transcripts characterization in Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Agrobacterium tumefaciens plasmid pTiA6NC. Bacteria; Proteobacteria;

Proteobacteria;

alpha subdivision;

Rhizobiaceae

update

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OF REAL COCCOCCOCCETTE NAME OF STREET NAME OF STREE
TRAM_AGRT6 Length: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                   KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MUZAKI A., NAKAZAKI N., NARUO K.,
KIMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
YAMADA M., YASUDA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
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"Activity of the Agrobacterium Ti plasmid conjugal transfer re
Tran is inhibited by the product of the tram gene.";

J. Bacteriol. 177:1367-1373(1995).

-i- FUNCTION: NEGATIVELY REGULATES CONJUGATION AND TRA GENES

-i- EXPRESSION BY ANTAGONIZING TRAR/AAI DEPENDENT ACTIVATION.

EITHER BIND OR MODIFY TRAR OR AAI MAKING THEM UNAVAILABLE.

ALTERNATIVELY, TRAM MAY BIND TRA PROMOTERS PREVENTING TRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE;
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modified and this statement is not remov-
entities requires a license agreement (So
or send an email to license@isb-sib.ch).
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRNA (GUANINE-N1)-METHYLTRANSFERASE (EC 2.1.1.31)
METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)
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EMBL; U16786; AAA64838.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE. TRNA - S-ADENO:
L-HOMOCYSTEINE + TRNA CONTAINING N(1)-METHYLGUANINE.
SUBCELLULAR IOCATION: CYTOPLASMIC (POTENTIAL).
SINIIARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMD FAMILY
                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
CATALYTIC ACTIV
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of the tram gene.";
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IP TRMU_YEAST
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE
(EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D90901; BAA16843.1;
Transferase; Methyltransfe
SEQUENCE 231 AA; 25949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BROWN D., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
Submitted (SEP-1997) to the EMBL/CHEBALK/DDBJ databases.
-i-CATALYTIC ACTIVITY: S-ADENOSYL-L-METH/IONINE + TRNA = S-ADENOSYL-L-
HOMOCYSTEINE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAC23H4.04.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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                                            401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                           EMBL; Z98977; CAB11659.1; -
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                                                                                                                                                                                                                                                                                                                               e; Methyltransferase; tRNA processing.
415 AA; 47626 MW; 36B7C485 CRC32;
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
                                                                                                                                                   01-OCT 1996 (Rel. 34, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
01-OCT 1996 (Rel. 34, Last sequence update)
01-OCT 1996 (Rel. 34, Last annotation update)
TROPINONE REDUCTASE HOMOLOG (EC 1.1.1.-) (P29X).
Datura stramonium (Jimsonweed) (Common thornapple).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                        401
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NARAJIMA K., HASHIMOTO T., YAMADA Y.;
"Two tropinone reductases with different stereospecificities short-chain dehydrogenases evolved from a common ancestor.";
Proc. Natl. Acad. Sci. U.S.A. 90:9591-9595(1993).
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EMBL; Z74081; CAA98591.1; -.
Transferase; Methyltransferase; trNA processing.
SEQUENCE 417 AA; 47049 MW; 4690E911 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAULIN L., SAREN A.M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA - S-ADENOSYL-L-HOMOCYSTELNE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                         TISSUE-ROOT
                                                                                                       SEQUENCE FROM N.A.
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales:
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(EC 2.1.1.61).
YDL033C OR D2761.
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Rel. 36, Last sequence update)
Rel. 36, Last annotation update)
(5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                     STANDARD;
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!!AA_SEQUENCE 1.0
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EMBL; M74901; AAA51445.1; -.
PIR; JN0451; JN0451.
HSSP; Q56320; INSJ.
PFAM; PF00218; IGPS; 1.
PFAM; PF00278; IGPS; 1.
ISOMETASS; TYPETOPHAN biosynthesis
SEQUENCE 312 AA; 33070 MW; C5A
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     Cryptococcus neoformans (Filobasidiella neoformans)
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tre
Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
N-(5'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE (EC 5.3.1.24) (PRAI).
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HSSP; P19922; ZHSD.
PROSITE; PS000061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
PFAM; PF00678; adh_short_C2; 1.
Oxidoreductase; NADP;
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FAMILY (SDR).
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167
268 AA;
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167
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the European Bioinformatics Institute. Their
use by non-profit institutions as long a
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Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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TRANSFAC; T02098; ...
PROSITE; PS00027; HOMEOBOX_2;
PROSITE; PS50071; HOMEOBOX; 1.
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MEDLINE; 96034516.
VAN RENTERGHEM P.H.G.,
"Study of TTF-1 gene e:
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1)
(HOMEOBOX PROTEIN NKX-2.1)
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X77910; CAA54868.1;
HSSP; P23441; 1FTT.
                                                                                                                                                                                                            DNA_BIND
                                                                                                                                                                                                                                                                                Transcription
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Ceil Endocrinol 112:83-93(1995).
FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROTD SPECIFIC GENES SUCH AS THYROGLOBULIN, THYROPEROXIDASE, AND THYROTROPIN RECEPTOR. CRUCIAL IN THE MAINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLROLE IN LUNG DEVELOPMENT AND SURFACTANT HOMEOSTASIS.
SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: THYROID, LUNG AND CNS.
TISSUE SPECIFICITY: THYROID, LUNG AND CNS.
SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
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    February 14,
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                                                                            MW:
                                                                                                                                                                                                                                                                                Activator; Homeobox; DNA-binding;
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                                                                                                        POLY-GLN.
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                                                                                                                                                                                                            HOMEOBOX
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    08:02 Type:
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                                                                        CRC32;
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101

QDTMRNSASG PGWYGANPDP

RFPAISRFMG TAAGVPQLSH

PASGMNMSGM SAVGGYCNGN GGGLGAPLAA

GGLGSLGDVS

51

AAMQQHAVGH MSMSPKHTTP

HGAVTAAYHM FSVSDILSPL

EESYKKVGME

YRQGQAAPPA

LGNMSELPPY

μ

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MEDLINE; 95229(
IKEDA K., CLARK
WHITSETT J.A.;
"Gene structure
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 use by modified
                                                                                  TTF1_HUMAN STANDAR: PRT: 371 AA.

P4369; O14955; O14954;

01-NOV-1995 (Rel. 32, Created)

101-NOV-1995 (Rel. 32, Last sequence update)

101-NOV-1995 (Rel. 38, Last annotation update)

15-UUL-1999 (Rel. 38, Last annotation update)

THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1)
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-LUNG;
HAMDAN H., LIU H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-THYROID;
MEDLINE; 95226464.
SAIARDI A., TASSI V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOMEOBOX PROTEIN NKX-2.1).
TITF1 OR TTF1 OR NKX2A.
                                                                                                                                                                                                                                                                                                                TISSUE-LUNG;
HAMDAN H., LIU H., JONES
Submitted (OCT-1995) to t
                                                                                                                                                                                                                                                                                                                                                                                                HAMDAN H., LIU H., DELEMOS I
Submitted (JAN-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGUCHI H., KIMURA S.
Submitted (JAN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 95229626.
IKEDA K., CLARK J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSSGSDYGTM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure and expression of human thyroid transcription r-1 in respiratory epithelial cells."; ol. Chem. 270:8108-8114(1995).
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e EMBL/GenBank/DDBJ
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IIAA_SEQUENCE 1.0

ID TTF1_MOUSE
AC P50220;

DT 01-0CT-1996 (R
DT 01-0CT-1996 (R
DT 01-0CT-1999 (R
DT 15-UUL-1999 (R
DE THYROLID-TRANSC
DE (HOMEOBOX PROT
GN TIF1 OR TTF1
OS MUS MUSCULUS
(OC EUKARYOTA; Met
OC THANOLOGIA
RT "The Complete
RT enhancer bind:
RT deduced amino
RL Biochim. Biop)
CC -1-FUNCTION:
CC THYROPERO;
CC THYROPERO;
CC MAINTENAN(
N [1]

P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RC STRAIN-129/SV; TISSUE-LIVER;

RC STRAIN-129/SV; TISSUE-LIVER;

RX MEDLINE; 95226463.

RA OGUCHI H., PAN Y.T., KINURA S.;

RT onhancer-binding protein (T/EBP) gene: extensive identity of the enhancer-binding protein (T/EBP) gene: extensive identity of the deduced amino acid sequence with the human protein. The deduced amino acid sequence with the human protein. The BIOCHIM. Biophys. Acta 1261:304-306(1995).

CC -1- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE PROMOTER OF THYROID SPECIFIC GENES SUCH AS THYROGLOBUIN, THYROID SPECIFIC GENES SUCH AS THYROGLOBUIN, THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY A
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EMBL; U19816; AAC50125.1; -.
EMBL; U19756; AAA86099.1; -.
EMBL; U43203; AAA89066.1; ALT_INIT.
EMBL; U33749; AAA852381.1; -.
EMBL; D50740; BAA252529.1; -.
EMBL; D50740; BAA23527.1; -.
EMBL; D50739; BAA23527.1; -.
EMBL; D50739; BAA23527.1; -.
EMBL; D50740; BAA23527.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UU-1996 (Rel. 38, Last annotation update)
THYROID-TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1)
(HOMEDBOX PROTEIN MKX-2.1).
TITF1 OR TITF1 OR NKX2-1 OR NKX-2.1.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; (
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GWYGANPDPEPAI -> V (I GWYGANPDPEPAI -> V (I REF. 6).

P -> H (IN REF. 6).

H -> P (IN REF. 6).

S -> T (IN REF. 6).

R -> G (IN REF. 6).

R -> G (IN REF. 5).

W; FEA215E7 CRC32;
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MEDLINE; 95071477.

ENDO T., OHTA K., SAITO T., HARAGUCHI K., NAKAZATO M., KOGAI CONAYA T.;
                                                                                                                                                                                                "Thyroid nuclear factor 1 (TTF-1) a novel DNA binding specificity."; EMBO J. 9:3631-3639(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTFI_RAT

P23441; O08630; O70121;

01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-UIL-1999 (Rel. 38, Last annotation update)
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLE:
(HOMEDOX PROTEIN NXX-2.1).
TITFI OR TTFI OR TTF-1 OR NXX-2.1.
TITFI OR TTFI OR TABLE.
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-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: THYROID, LUNG AND BRAIN.
-!- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
-!- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
-!- SIMILARITY: BELONGS TO THE NK-2 FAMILY OF HOMEOBOX PROTEINS.
-!- SIMILARITY: BELONGS TO THE STATE AND THE STATE AND THE STATE AND THE SUBSECTION OF THE SWISS INSTITUTE OF BIOINFORMATICS and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              GUAZZI S., PRICE M.,
DI LAURO R.;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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W; E047C32A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACTOR 1) (TTF-1)
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Rattus.
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(TTF-1) gene.";

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STITITES REPRESENTATION OF THE PROCESS OF THE PROCE
ID TXF8_DENAN
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A LEDONARDI A., DI LAURO R., VIGLINO P.;
A LEONARDI A., DI LAURO R., VIGLINO P.;
ANALYSIS OF The SOLUTION STRUCTURE OF The homeodomain of rat thyroid
at transcription factor 1 by 1H-NMR spectroscopy and restrained
at molecular mechanics.",
THE LOYALTION THAT BINDS AND ACTIVATES THE
C. I. SHOCHEM. 241:101-113(1996).
THE FUNCTION: TRANSCRIPTION FACTOR THAT BINDS AND ACTIVATES THE
PROMOTER OF THEFULD SPECIFIC GENES SUCH AS THYROGLOBULIN,
THYROPEROXIDASE, AND THYROTROPIN RECEPTOR. CRUCIAL IN THE
ANINTENANCE OF THE THYROID DIFFERENTIATION PHENOTYPE. MAY PLAY A
C. ROLE IN LUNG DEVELOPMENT AND SURFACTANT HOMEOSTASIS.
C. I. SUBCELLULAR LOCATION: NUCLEAR.
C. I. SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Structural study of rat thyroid tra (TTF-1 HD) by nuclear magnetic reson FEBS Lett. 336:397-402(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE
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EMBL; D38035; BAA07231.1; ALT_SEQ.
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Nuclear protein; 3D-struct
DNA_BIND 161 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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                                                                                                       LNSSGSDYGA
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TE; PS50071; HOMEOBOX_2; 1.
PF600046; homeobox; 1.
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372 AA;
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29-JAN-96.
   STANDARD
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                                                                                                                                                                                                                                                                                                                                                                             RRKRRVLFSQ
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220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38554 MW;
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; AEOF1572 CRC32;
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   PRT;
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  resonance.";
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                                                                                                                                                                      LAHHAASPAA
                                                                                                                                                                                                                                      ASLQGHAQQQ
                                                                                                                                                                                                                                                                                                         ODSGGGGGG
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IIIAA_SEQUENCE 1.0

ID UBC7_DROME

AC P52487;

DT 01-CCT-1996 (R

DT 01-CCT-1996 (R

DT 01-NOV-1997 (R

DE LIGASE) (UBIOU

GN UBC84D;

OS Drosophila mel

OC Eukaryota; Met

OC Ephydroidea; E

RM GIJUNCE FROM

RA ROBIN C., MEDV
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DISULFID
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CONFLICT
SEQUENCE
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21-JUI-1986 (Rel. 01, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
TOXIN F-VIII PRECURSOR (TOXIN TAZ) (TOXIN DAFS).
Dendroaspis angusticeps (Eastern green mamba).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
                                                                                                             UBIQUITIN-CONJUGALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venom;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE; 74070661.

VILLODEN C.C., BOTES D.P.;

VILLODEN C.C., BOTES D.P.;

VISHARE VENOM toxins. The purification and amino

VISHARE VENOM DENDROSAPIS angusticeps Venom.";

J. BIO1. Chem. 249:366-372(1974)

-I- FUNCTION: ITS PHARMACOLOGICAL ACTION IS UNKN
   SEQUENCE FROM N.A. ROBIN C., MEDVECZKY
                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; H
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A01675; T5EP2A.
PIR; S211299; S211299.
HSSP; P01416; INTX.
PROSITE; PS00272; SNAKE TOXIN;
PFAM; PF00087; toxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X53409; CAA37485.1; -.
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TISSUE-VENOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-VENOM GLAND; DUCANCEL F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: LD(50) IS >250 MG/KG BY SUBCUTANEOUS INJECTION.
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                                                                                                                                                                                                                                                       LPAIVAGRGC GCPSKEMLVA IHCCRSDKCN
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FID 38
FID 38
FID 74
FID 74
                                                                                                                                                                                                                                                                                                               Length: 81
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                                                                                                                                                                                                              STANDARD;
                                                                                                                      CARRIER PROTEIN).
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   RUSSELL R.J.,
                                                                                                                                                                                                                                                                                                                                           TOXIN F-VIII.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
I -> V (IN REF.
EOBFC94E CRC32;
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     OAKESHOTT
                                                                                                                                                                                                              8
                                                            Hexapoda; Ins
a; Brachycera;
                                                                                                                                                                                                                                                                                                              Type: P
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                                                             Muscomorpha;
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THE REAL PROPERTY OF THE PROPE
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SEQUENCE FROM N.A.
MEDLINE: 85242679.
MEDLINE: AKABOSHI E., SHINAGAWA H., HORII T., OG
KITAGAWA Y., AKABOSHI E., SHINAGAWA H., HORII T., OG
"Structural analysis of the umu operon required for
"Structural analysis of the umu operon required for
mutagenesis in Escherichia coli.";
mutagenesis in Ford. Sci. U.S.A. 82:4336-4340(1985).
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01-NOV-1986
15-JUL-1999
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-- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN PROTEINS (BY SIMILARITY).

-- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + PYROPHOSPHATE + PROTEIN N'UBIQUITYLLYSINE.

-- PARHMAY: SECOND STEP IN UBIQUITIN CONJUGATION.

-- PARHMAY: SECOND STEP IN UBIQUITIN TREDUTED FOR UBIQUITIN-THIOLESTER FORMATION (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE UBIQUITIN CONJUGATING ENZYME STRONGEST, TO HUMAN UBC7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U51051; AAB01150.1; -.
HSSP; P15731; 2UCE.
FLYBASE; FBGR0017456; Ubc84D.
PROSITE; PS00183; UBIQUITIN_CONJUGAT;
PFAM; PF00179; UQ_con; 1.
Ub1quitin conjugation; Ligase.
Ub1QUITIN
BINDING 86 86 UBIQUITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
STRALN=K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYKEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                MEDLINE; 85242678.

PERRY K.L., ELLEDGE S.J., MITCHELL B.B., MARSH L., PERRY K.L., ELLEDGE S.J., MITCHELL B.B., MARSH L., "umuDC and mucAB operons whose products are requirated mucDc and chemical-induced mutagenesis: UmuD, MucA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
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(Rel. 03, Last sequence update)
(Rel. 38, Last annotation update)
N (EC 3.4.21.-) [CONTAINS: UMUD' P)
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41698C20 CRC32;
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UMUD_ECOLI
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EMBL; M10107; AAA28728.1; -.
EMBL; AE000216; AAC74267.1; -.
EMBL; D90752; BAA36030.1; -.
EMBL; D90752; BAA36038.1; -.
PIR; A03551; ZWECD.
PIR; A23157; A23157, PDB; 1UMU; 01-AUG-96.
PDB; 11MU; 01-AUG-96.
PDB; 1AY9; 28-JAN-98.
ECOZDBASE; A015.1; 6TH EDITION.
ECOZDBASE; A015.1; 6TH EDITION.
ECOZDBASE; A015.1; 6TH EDITION.
ECOZDBASE; A015.1; 6TH EDITION.
SCONUTAGENESSE; DNA TEPPAIR; AUTOCATALYTIC CLESSENTED PFAM; PFOOTOTS; DNA TEPPAIR; AUTOCATALYTIC CLESSENTED PFAM; POOTOTS; 
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MEDLINE; 97061202.
MEDLINE; 97061202.
OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A.,
OSHIMA T., AIBA H., BABA T., FUJITA K., HAYASHI K., KASHIMOTO K.,
IKEMOTO K., INADA T., ITOH T., KAJHIMARA M., KANAI K.,
KIMURA S., KITAAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K.,
MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., SAITO N.,
SAMPEI G., SEXI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y.,
YANO M., HORIUCHI T.;
YANO M., HORIUCHI T.;
YA 7.18-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                            PROPEP
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[4]
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11 FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION. ESSENTIAL FO INDUCED (OR SOS) MUTAGENESIS. MAY MODIFY THE DNA REPLICATION MACHINERY TO ALLOW BYPASS SYNTHESIS ACROSS A DAMAGED TEMPLATE.

1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S24 ALSO KNOWN AS THE UMUD/LEXA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 96202734.

PEAT T.S., FRANK E., MCDONALD J.P., LEVINE A.S., WC HENDRICKSON W.A.;
"Structure of the UmuD' protein and its regulation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF UMUD'.
MEDLINE; 96202734.
PERIT I.S., FRANK E., MCDONALD J.P., LEVINE A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleavage.
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  Length: 139
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ENNIS D.G.,
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C mutants: DNA
                                                MW;
                                        UMUD' PROTEIN.

CLEAVAGE (AUTO-).

INVOLVED IN AUTO-CLEAVAGE.

INVOLVED IN AUTO-CLEAVAGE.

P->D: IN UMUD1; NON-CLEAVABLE.

G->R: IN UMUD1; NON-CLEAVABLE.

G->D: IN UMUD7; NON-CLEAVABLE.

MW; D0175DFA CRC32;
14, 2000
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  Type: P
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TYFVKASGDS MIDGGISDGD LLIVDSAITA SHGDIVIAAV DGEFTVKKLQ

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MLFIKPADLR

EIVTEPLESD

LVQCGFPSPA

ADYVEORIDL

NOLLIGHPSA

LRPTVQLIPM

NSAYSPITIS

SEDTLDVFGV VIHVVKAMR

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II AA_SEQUENCE 1
ID VANS_ENTER
AC Q06240;
DT Q1-QCT-199
DT Q1-DEC-199
DT 15-DEC-199
DE SENSOR PRC
DE (VANCOMYCI)
GN VANS.
OS Enterococo
OG Plasmid pl
OC Bacteria;
OC Enterococo
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Q06240;
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01-OCT-1993
01-JUN-1994
01-FEB-1996
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                            01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SENSOR PROTEIN VANS (EC 2.7.3.-) (VANCOMYCIN (VANCOMYCIN HISTIDINE PROTEIN KINASE).
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PIR; A44215; A44215.
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"Open reading frames encoding a protein kinas, homolog of
glycoprotein gx of pseudorables virus, and a novel glycoprotein
within the unique short segment of equine herpesvirus type 1.",
virology 188:545-557(1992).

"IT SIMILARITY: BELONGS TO THE HERPESVIRUSES US2 FAMILY.
                                                    Enterococcus faecium (Streptococcus faecium).
Plasmid pIP816.
Bactería; Firmicutes; Bacillus/Clostridium group;
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(Rel. 29, Last sequence update)
(Rel. 33, Last annotation update)
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RP RN COS
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P36778;
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EMBL; M68910; AAA24788.1; -.
PFAM; PFO0512; signal; 1.
Sensory transduction; Transferase; Kinase; Transmembrane; Cell Antibiotic resistance; Phosphorylation; Plasmid.
Antibiotic resistance; Phosphorylation; Plasmid.
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SEQUENCE
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-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM VANS/VANR.

-CTIVATES THE TRANSCRIPTION OF VANH, VANA AND VANX IN RESPONSE TO VANCOMYCIN WHICH RESULTS IN VANCOMYCIN RESISTANCE. VANS ACTIVATES VANR BY PHOSPHORYLATION.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
REGULATORY PROTEIN E2.
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BM4147.";
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ARTHUR M., MOLINAS C., COURVALIN P.;

The Vans-Vank two-component regulatory system controls synthesis arthur vans-Vank two-component regulatory system controls synthesis are vans-vank two-component regulatory system controls synthesis.
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"Characterization of Ini346, a In3-related transposon conferring
glycopeptide resistance by synthesis of depsipeptide peptidoglycan
precursors in Enterococcus faccium BM4147.";
J. Bacteriol. 175:117-127(1993).
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                           Human papillomavirus type
Viruses; dsDNA viruses, n
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 SEQUENCE FROM N.A.
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76
164
384 AA;
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164
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PHOSPHORYLATION (AUTO-)

89EA01F7 CRC32;
                               stage;
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                             Papovaviridae;
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                               Papillomavirus
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IIAA_SEQUENCE 1.0
ID VE2_HPV10
AC P36781;
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DELIUS H., HOFMANN B.;

Primer directed sequencing of human papillomavirus types.";

"Primer directed sequencing of human papillomavirus types.";

CUTT. Top. Microbiol. Immunol. 186:13-31(1994).

CUTT. Top. Microbiol. Immunol. TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCUNUNUNGGT-3') PRESENT MULTIPLE COPIES IN THE REGULATION IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA REPLICATION.

-I. SUBURIT: BINDS DNA AS A DIMER.

-I. SUBURIT: BINDS DNA AS A DIMER.
DELIUS H., HOPMANN B.;

DELIUS H., HOPMANN B.;

Primer-directed sequencing of human papillomavirus types.";

Primer-directed sequencing of human papillomavirus types.";

Curr. Top. Microbiol. Immunol. 186:13-31(1994).

-i. FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNNNINNINGGT-3') PRESENT

IN MULTIPLE COPIES IN THE RECULATION REGION. IT CAN EITHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
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PIR; S36552; S36552.
HSSP; P17383; 1DHM.
PFAM; PF00518; EZ_N; 1.
PFAM; PF00511; EZ_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 383 AA; 44246 MW; CFBD1DEA CRC32;
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                                                                                                                                                                                                                                                 Human papillomavirus type 1
Viruses; dsDNA viruses, no
[1]
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat REGULATORY PROTEIN E2.
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o RNA stage; Papovaviridae;
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ID VE2_HPV18
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                                          REVISION TO 90.

REVISION TO 90.

REDITINE; 93197122.

"TaqI is a single cut enzyme for HPV-18.";

"TaqI is a single cut enzyme for HPV-18.";

"TaqI is a single cut enzyme for HPV-18.";

"TaqI is Acids Res. 21:1041-1041(1993).

"I BINDS TO THE E2RE RESPONSE ELEMENT' (5' ACCUNNUNGGT-3') PRES

IN MULTIPLE COPIES IN THE REQULATORY REGION. IT CAN ENTHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENT'S. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DN

INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DN
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PIR; S36535; S36535.
HSSP; P17383; 1DMM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early Protein; Transcription regulation; Activator; DNA-binding; Transcription regulation; Repressor; Nuclear protein SEQUENCE 376 AA; 43003 MW; 799683D3 CRC32;
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                                                                                                                                                                                                                                                                    "Nucleotide sequence and comparative analysis of the human papillomavirus type 18 genome. Phylogeny of papillomaviruses repeated structure of the E6 and E7 gene products.";
J. Mol. Biol. 193:599-608(1987).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 87283882. COLE S.T., DANOS O
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
REGULATORY PROTEIN E2.
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P06790;
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SUBUNIT: BINDS DNA AS
SUBCELLULAR LOCATION:
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es; dsDNA viruses, n
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PIR; D26251; WAWL18.
HSSP; P17383; IDHM.
PFAM; PF00518; E2_N; 1.
EFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 365 AA; 41294 MW; 1871C1FE CRC32;
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                                                                                                                                                                                                            EMBL; U31783; AAA79425.1; --.
HSSP; P17383; 1DHM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00551; E2_C; 1.
SEQUENCE 376 AA; 43234 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
101
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                                                                                                                                                        Length: 376
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28; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus
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(Rel. 34, Last annotation update)
PROTEIN E2.
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43234 MW;
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VE2_HPV2A

Length: 391

151 101

SVSSTQASAS

DDEPLSPIRT YVHDGVRVNY

AVSPVPAPVA ASAESTGAGR AAPPTQALCS

RWGHGDTDSV

PVIHLRGDAN

CLKCFRYRVQ

KHKDVLYARV SSTWHWAGGN

EGEVECYNKR SISDSNRTDP

RORVIVGOOH

PRPDSTRTVG

YTSVEQRTEF

LTRVSIPKGL IALPGYMSAF

51 ш

ALTVSKAKAC

QAIEVQLALQ

TLMQSAYSTE AWTLRDTCLE

MWDAPPKKCW KKKGQSVLVK FDGSSDRDMI YTSWGFIYVQ DTITDSWHKV

VDFGTESLTY

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AGTVIHHTSA

METLANRIDA CQETILIELYE KDSNKLEDQI KHWAQVRLEN VMLFKARECG

February 14, 2000 08:02 Type:

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ID VE2_HPV2A
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                                                                                                                                                                                                                                                                                                                                                                                                                   HIRSCH-BEHNAM A., DELIUS H., DE VILLIERS E.M.;
"A comparative sequence analysis of two human papillomavirus (HPV)
types 2a and 57.";
Virus Res. 18:81-98(1990).
-I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION
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HSSF; P17383; 1DHM.

PFAM; PF00508; E2_N; 1.

PFAM; PF00518; E2_C; 1.

PFAM; PF00511; E2_C; 1.

Early protein; Transcription regulation; Activator; DNA-binding; Transcription; Pepressor; Nuclear protein.

SEQUENCE 391 AA; 43233 MW; B3DF7AF6 CRC32;
                                                                                                               EMBL; X55964; -; NOT_ANNOTATED_CDS.
                                                                                                                              use by non-profit institutions as ro
modified and this statement is not remo
entities requires a license agreement is
or send an email to license@isb-sib-ch)
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MEDLINE; 91188699.
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01-MAY-1992 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iruses;
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iruses; dsDNA viruses, no R
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                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                        FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BLODS TO THE E2RE RESPONSE ELEMENT (5 -ACCNNNUNGGT-3') PRESEI
IN MULTIPLE COPIES IN THE REGULATION REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
BY INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                                                                                           REPLICATION.
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annotation
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THE PROPERTY AND THE PROPERTY OF SOLUTIONS OF THE PROPERTY OF THE PROPE
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VE2_HPV31
P17383;
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Biochemistry 35:2095-2103(1996).

-I - FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

-I - FUNCTION: E2 RESPONSE ELEMENT (5'-ACCUNUNUNGGT-3') PRESENT IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION
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PIR; D32444; W2WL31.
PDB; 1DHM; 07-DEC-96.
PFAM; PF00508; EZ_N; 1.
PFAM; PF00511; EZ_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein
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LIANG H., PETROS A.M., MEADOWS R.D., YOON H.S., EGAN D.A., WIHLDANG H.T., ROBINS T., FESIK S.W.;
"Solution structure of the DNA-binding domain of a human papillomavirus E2 protein: evidence for flexible DNA-binding papillomavirus E2 protein: evidence for flexible DNA-binding
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01-AUG-1990 (Rel.
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Viruses; dsDNA viruses, no
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SUBCULTULAR LOCATION: NUCLEAR.
SUBCELLULAR LOCATION: NUCLEAR.
DDFLNTVKIP
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                                                     DANILKCLRY
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NTVSVSTGYM
                                                     RLSKYKQLYE QVSSTWHWTC
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15, Last sequence update)
36, Last annotation update)
N E2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42104 MW; B34B2CC1 CRC32;
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                                                     TDGKHKNAIV
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ID VE2_HPV45
AC P36794;
                                            P26541;

P26541;

01-AUG-1992 (Rel. 23, C)

01-AUG-1992 (Rel. 23, L)

15-UUL-1998 (Rel. 36, L)

15-UUL-1998 (Rel. 36, L)
Human papillomavirus type 5
Viruses; dsDNA viruses, no
[1]
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PIR; S36564; S36564.
HSSP; P17383; DLHM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; DNA-binding;
Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SEQUENCE 368 AA; 41946 MW; 7D4616A6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                           351
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01-JUN-1994 (Rel. 29, Last seq
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REGULATORY PROTEIN E2.
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                                                                                                                                           DVVTIPNSVQ
                                                                                                                                                                  NSLKCLRYRL
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Last sequence up
Last annotation
            RNA stage; Papovaviridae; Papillomavirus.
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annotation updat
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VE2_HPV51
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BIOLOGIC properties and nucleotide sequence analysis

Biologic properties type 51.",

papillomavirus type 51.",

J. Virol. 65:4216-4225 (1991).

-I- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.

IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCUNUNUNGGT-3') PRESENT

IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER

ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING OF E2RE'S POSITION

WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

BY STERICALLY HINDERING THE ASSEMBLY OF THE TRANSCRIPTION

BY STERICALLY HINDERING THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
                                                                                                                                                                                                                                         P36796;
01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                           _SEQUENCE 1.0
VE2_HPV52
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"Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-i- FUNCTION: E2 RESQUATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACCNUNUNUNGGT-3') PRESENT
IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
ACTIVATE OR REPRESS TRANSCRIPTION DEPRENDING OF E2RE'S POSITION
WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
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PIR; B40415; W2WL51.

HSSP; P17383; 1D4M.

PFAM; PF00508; E2_N; 1.

PFAM; PF00511; E2_C; 1.

Early protein; Transcription regulation; Activator; DNA-binding; Trans-acting factor; DNA replication; Repressor; Nuclear protein; SEQUENCE 358 AA; 40908 MW; E0C9694E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
MEDLINE; 91303675
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                                                                                                                                                                                                                              REGULATORY PROTEIN
                                                                                                            DELIUS H., HOFMANN B.;
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                                                                                                                                                                              iruses; dsDNA viruses, no
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LAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                                                                                                           PRT;
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PIR; S36576; S36576.
HSSP; P17383; 1DHM.
PFAM; PF00508; E2_N; 1.
PFAM; PF00511; E2_C; 1.
Early protein; Transcription regulation; Activator; Trans-acting factor; DNA replication; Repressor; Nuc SEQUENCE 368 AA; 41739 MW; 918AE9D9 CRC32;
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                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 94018622.
WULFF D.L., HO Y.S., POWERS S., ROSENBERG M.;
"The int genes of bacteriophages P22 and lambda are regulated different mechanisms.";
MOI. Microbiol. 9:261-271(1993).
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  EMBL; L06296; AAC18882.1;
PIR; S35282; S35282.
SEQUENCE 317 AA; 35719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage P22.
Viruses; dsDNA viruses,
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VEAA_BPP22
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SUBUNIT: BINDS DNA AS A DIMER.
SUBCELLULAR LOCATION: NUCLEAR.
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clear protein
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VEAA_BPP22

Length: 317

35719 MW; 0 February 14,

Туре:

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Check:

05933D59 CRC32;

51

MITITKERIE

TCVTLEQQPN AADDVAVYIP LYAAPPVPER ERIRREHAEW

LFVKSPLENG LTRGEQMELA RIALASLDAE TVRYLNKFSG

ALEAAADPSD PLEWADMQFL

LWDAQRRMGI VPEECPAELP

SDEFITRAMI

SDKTFGDVGP

151 201

YALCWOSGEV

TIWINNYSGT

CVQEYVKLER

LQEALAGNSP

LHIKEQPESV

YAQVKAVADI

VGPLKHLSKE EKLEINKTRQ

VIPGGWISCS

WPEPKDGEPR VTYTPDPEKA ERMPDNDESK

PIAIFTGKCL

GQGMFVATYD DDGFFDYWEG

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EMBL; J02454; AAA32324.1; -.
EMBL; V00657; CAA24020.1; -.
EMBL; M25080; AAA32328.1; -.
ETR; A04252; ZGBPG4.
PDB; IGFF; 03-APR-96.
COAL PROTEIN: 3D-Structure.
COAL PROTEIN: 3D-Structure.
                                                                                                                                                                                           VGG_BPG4
                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsib.ch).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MAJOR SPIKE PROTEIN (G PROTEIN) (GPG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                "Site-specific initiation of a DNA fragment: nucleotide sequence the bacteriophage 64 negative-strand initiation site."; Proc. Natl. Acad. Sci. U.S.A. 75:3094-3098(1978).
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 78240755.
SIMS J., DRESSLER D.;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 79053264.
GODSON G.N., BARRELL B.G., STADEN R.,
"Nucleotide sequence of bacteriophage
Nature 276:236-247(1978).
             Coat protein;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-81 FROM N.A.
                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
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177 AA;
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700A8E43 CRC32;
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G4 DNA.";
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VGG_BPG4

Length:

177

February

14,

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Type: P

Check: 4484

51

TTHSGLCHVV

MFQKFISKHN APINSTQLAA TKTPAVAAPV LSVPNLSRST ILINATTTAV

RIDETNPTNH HALSIAGSLS NVPADMIAFA IRFEVADGVV

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USEQUENCE 1.0
VGLM_HSVSA
Q01017;

STANDARD;

PRT;

366 AA

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101 151 201 251 301 351

TPGASRPTPP
SRHRLTVAQV
GVSCAVNEAA
GPVVLLSVSP

RPRSGPTAPQ

MARLGAELRS HPNTPPKPRR RSSSSTTMPS LTSIAEESEP

VGLI_HSV2H

Length: 372

51

LRVFGELHFV

PAVAFTICRS THHAHSPAYP TLELGLARQP LLRVRTATRD YAGLYVLRVW

RTTTPPSSPR DPTPAPGDTG

TPAPASGEIA FIHRCQRRYR

IQIAIPASII

AFVFLGSCIC

APRIGPSSYY
PPNSTRSASE
RPRGQIYNPG

VLGVALSANG

TFVYNGSDYG

SCDPAQLPFS

MPGRSLQGLA ILGLWVCATG LVVRGPTVSL VSDSLVDAGA VGPQGFVEED

February 14, 2000 08:02 Type: P Check:

501

GAQVPHINYY DGIIELFHYP LGNHCPRVVH

VVTLTACPRR

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                                                                                      EMBL; X04798; CAA28485.1; -. EMBL; Z86099; CAB06714.1; -. PIR; F43674; F43674.
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus (type 2 / strain Viruses; dsDNA viruses, no RNA stage; Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                                                                                                                                                                            MCGEOCH D.J., MOSS H.W.M., MCNAB D., FRAME M.C.;
"DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary comparisons.";
                                                                                                                                                                                                                                                                                                         Submitted (FEB-1997)
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01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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                                                                           lycoprotein
                                                                                                                                                                                                                                                                                                                                                            Gen. Virol. 68:19-38(1987).
                                                                                                                                                                                                                                              MISCELLANDOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 2: GH, GB, GC, GG, GB, GI, AND GE. SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GPI AND OPRV GP63.
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Herpesviridae;
           CRC32;
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01-OCT-1996
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TRANSMEM 17
TRANSMEM 152
TRANSMEM 152
TRANSMEM 214
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VIB8_AGRT5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the herpesvirus saimiri genome.";
J. Virol. 66:5047-5058(1992).
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NEWMAN C., WITTMANN S., (
HONESS R.W.;
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                                     Agrobacterium tumefaciens plasmid priC58. Bacteria; Proteobacteria;
                                                                                                VIRB8 PROTEIN
VIRB8.
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01-NOV-1990 (Rel. 16,
01-NOV-1990 (Rel. 16,
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-1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
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Viruses; dsDNA viruses, no F
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                  Proteobacteria; alpha eae; Agrobacterium.
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                                          Rhizobiaceae group;
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MEDLINE; 90318324.

KULDAU G.A., DE VOS G., OWEN J., MCCAFFREY G., ZAMBRYSKI P.;
KULDAU G.A., DE OF VOS G., OWEN J., MCCAFFREY G., ZAMBRYSKI P.;
"The virb operon of Agrobacterium tumefaciens pTiC58 encodes 11 reading frames.";
Gen. Genet. 221:256-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A_SEQUENCE 1.0
VIB8_AGRT6
P09781;
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01-AUG-1991 (Rel.
15-DEC-1998 (Rel.
VIRB8 PROTEIN.
MEDLINE; 90.
WARD J.E., I
NESTER E.W.
J. Biol. Ch
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MEDLINE; 90301800.

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S., MOREL P.,

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S., MOREL P.,

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S., MOREL P.,

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S., MOREL P.,

"MOLECULAR CHARACTERIAT OF A POWELL SEQUENCE and gene organization of tumefaciens: complete nucleotide sequence and gene organization of tumefaciens complete nucleotide sequence and gene organization of tumefaciens complete nucleotide sequence and gene organization of the vir regular of tumefacients as a single unit.";

Plasmid 23:85-106(1990)

Plasmid 23:85-106(1990)

Plasmid 23:85-106(1990)

TRANSFER TO PLANT CELLS.
                                                                                                                                                     WARD J.E., AKIYOSHI D.E., REGIER D., MESTER E.W.;
"Characterization of the virB operon tumefaciens Ti plasmid.";
J. Biol. Chem. 263:5804-5814(1988).
                                                                                                                                                                                                                                                                                                                                                     Agrobacterium tumefaciens.
Plasmid pTiA6.
Pacteria; Proteobacteria; al
Bhizobiaceae; Agrobacterium.
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CONFLICT 21 22
CONFLICT 128 129
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237 AA;
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SA -> TR (IN REF. 2);
CD671958 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                            subdivision;
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                                                        GORDON
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I !!AA_SEQUENCE 1.0
ID VIB8_AGRT9
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens.
Plasmid pT115955.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Agrobacterium.
[1]
                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   THOMPSON D.V., MEICHERS L.S., IDLER K.B., SHILPEROORT HOOYKRAS P.J.J.;
HOOYKRAS P.J.J.;
"Analysis of the complete nucleotide sequence of the tumefaciens viiB operon.";
Nucleic Acids Res. 16:4621-4636(1988).
-!- FUNCTION: VIRB PROTEINS ARE SUGGESTED TO ACT AT T SURFACE AND THERE PLAY AN IMPORTANT ROLE IN DIRECTRANSFER TO PLANT CELLS.
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01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-1992 (Rel. 22, Last annotation update)
VIRB8 PROTEIN.
                                             EMBL; X06826; CAA29
PIR; S00784; B8AG55
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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PIR; I28621; B8AGA6.
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                                                                X06826; CAA29978.1; ALT_INIT
tumor; Plasmid.
230 AA; 25408 MW; 870AF438 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor; Plasmid.
230 AA; 25382 MW; 44A8A66C CRC32;
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RIRLINPAGI VVTSYQTSED TVSNVGQGAP
                                                  VEVEHIASND VTPSTQQIRY KRTLVVDGKM PVVSTWTATV RYEKVTSLPG
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REDUINE, 89039712.

RA MEDLINE, 89039712.

RA HIRLYMA I., WURNNAKA I., OKA A.;

RA HIRLYMA I., WURNNAKA I., OKA A.;

RA HIRLYMA I., WURNNAKA I., OKA A.;

RT MOTOGRATICATION and characterization of the virCD genes from

RT MOTOGRATION INTROGRATION BY A. TUMBERACIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERACIENS INVOLVES THE TRANSFER

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERACIENS INVOLVES THE TRANSFER

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CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERACIENS IN FILE THE VIRD OPERON ENCODES A SITE

CC -!- FUNCTION: TUMOR FORMATION BY A. TUMBERACIENS THE WITHIN BOTH

CC AND INTEGRATION OF A DEFINITION OF TI PLASMID DNA

CC SPECIFIC ENDONUCLEASE THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH

CC 19 SPECIFIC ENDONUCLEASE THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH

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CC 19 SPECIFIC ENDONUCLEASE THAT CLEAVES AT A UNIQUE SITE WITHIN BOTH

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01-JAN 1990 (Rel. 13, Last sequence update)
01-JAN 1990 (Rel. 13, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1...)
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EMBL; X12867; CAA31350.1; -.
PIR; S06883; S06883.
Hydrolase; Nuclease; Endonuclease; Crown gall tumor; Hydrolase; T-DNA.

VID1_AGRRA Length: 147 AA; 147 February 14, 2000 08:02 Type: P Check: 16005 MW; 414FDDA0 CRC32;

Н MSQGSKPTSS DIAINQRVGA TVEGFRVVST RLRSAEYESF SHQARLLGLS

51 DSMAIRVAVR RIGGFLEIDA ETRHKMEAIL LSIGTLSSNI AALLSAYAEN

PIMDLEALRA ERIAFGESFA DLDGLLRSIL SVSRRRIDGC

!!AA_SEQUENCE 1.0 p18591; p06520;
01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1...) STANDARD; 147

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Rhizobiaceae; Bacteria; Proteobacteria; alpha eae; Agrobacterium. subdivision; Rhizobiaceae

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VIB8_AGRT9 Length: 230

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LRESYDADTA QYAYDLVSNF SAPTVRQDYQ QFFNYPNPSS

IATMVPLSRL VPVYLWIRPD GTVDSEVSIS

RLPATQEEAV VNASLWEYVR

HYKEVEAFQT

ARAKSARRLS

KIIAAVAAIA

ILGNVAQAFA

February 14, 2000 08:02 Type: P Check:

MOREL

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SEQUENCE FROM N.A.

MEDLINE; 90301800.

ROGOWSKY P.M., POWELL B.S., SHIRASU K., LIN T.-S.,

ZYPRIAN E.M., STECK T.R., KADO C.I.;

"Molecular characterization of the vir regulon of P
tumefaciens: complete nucleotide sequence and gene
the 28 63-kbp regulon cloned as a single unit.";

Plasmid 23:85-106(1990). Agrobacterium e organization

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VID1_AGRT5
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PRELIMINARY SEQUENCE F
MEDLINE; 85190558.
HAGIYA M., CLOSE T.J.,
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VID1_AGRT6
SEQUENCE FROM N.A.

MEDLINE: 88032822.

JAYASWAL R.K., VELUTHAMBI K., GELVIN S.B., SLIGHTOM J.L.;

JAYASWAL R.K., VELUTHAMBI K., GELVIN S.B., SLIGHTOM J.L.;

TOUBLE-stranded cleavage of T-DNA and generation of single-stranded

T-DNA molecules in Escherichia coli by a vilD-encoded

border-specific endonuclease from Agrobacterium tumefaciens.";

J. Bacteriol. 169:5035-5045(1987).

I- FUNCTION: TUMOR FORMATION BY A.TUMEFACIENS INVOLVES THE TRANSFER

AND INTEGRATION OF A DEFINED SEGMENT (T-DNA) OF TI PLASMID DNA

INTO THE PLANT NUCLEAR GENOME. THE VIRD OPERON ENCODES A SITE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of pTiC58 plasmid-encoded proteins for Agrobacterium tumefaciens.";
proc. Natl. Acad co.
                                                                                                                                             WADDLINE: 87028239.
YANOFSKY M.F., PORTER S.G., YOUNG
NESTER E.W.;
"The virD operon of Agrobacterium
endonuclease.";
Cell 47:471-477(1986).
                                                                                                                                                                                                                                                  Agrobacterium tumefaciens.
Plasmid pTiA6NC.
Bacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Agrobacterium.
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EMBL; M11311; AAA98365.1; ALT_SEQ.

EMBL; M33673; AAA52110.1;

PIR; A22666; A22666.

PIR; S11838; S11838.
                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1989 (Rel. 12, Last annotation update)
T-DNA BORDER ENDONUCLEASE VIRD1 (EC 3.1.-.-).
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VLF1_NPVOP

Length: 374

February 14, 2000 08:03 Type: P Check:

889

101

DKELKTIREK

EKNFMLKNAI

DTILNFIDSK IKLMNSDYVH

DRGLIRGAIV

KETLQLTINE

YTNAMNLPEF

SASRFEHVFD LATDRORCTP
IKIIFSLVEE ADLQNPAYDL

DREFDSVEFQ

51

MDGLGVRNET KYMFPKPFAP

TTLKSYKSRL

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VID1_AGRT6 Length:
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
AHRENS C.H., RUSSELL R.R., FUNK C.J., EVANS J., HARWOOD S.,
ROHRMANN G.F.;
"The sequence of the Orgyia pseudotsugata multinucleocapsid
"The sequence of the Orgyia pseudotsugata multinucleocapsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         polyhedrosis virus genome.";
Virology 229:381-399(1997).
-!- FUNCTION: INVOLVED IN VERY LATE GENE ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                      O10330;
01:NOV-1997 (Rel. 35, Created)
01:NOV-1997 (Rel. 35, Last sequence update)
01:NOV-1997 (Rel. 35, Last annotation update)
VERY LATE EXPRESSION FACTOR 1.
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EMBL; M17989; AAA22113.1;
PIR; A29826; A29826.
PIR; A25063; A25063.
                                                                                                                                                                                                                                                                                                                                                                                        Orgyia pseudotsugata multicapsid polyhedrosis virus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
   EMBL; U75930; AAC59079.1; -
PFAM; PF00589; Phage_integrase; 1.
Transcription regulation.
SEQUENCE 374 AA; 43165 MW; C56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Nuclease; Endonuclease; Crown gall tumor;
                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
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       C560A0FD CRC32;
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EIYARNPTVL QISKNTSTPF KDFRRLLDEA GVEMERPRSN

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VMA2_BRSVA Length: 186
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                                               two non-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZAMORA M., SAMAL S.K.;
"Sequence analysis of M2 mRNA of bovine respiratory syncytial virus obtained from an F-M2 dicistronic mRNA suggests structural homology with that of human respiratory syncytial virus.";
J. Gen. Virol. 73:737-741(1992).
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PIR: JO1482; WMNZBA.

PIR: JO1482; WMNZBA.

RATI'X PROTEIN; Envelope protein; Glycoprotein.

CARBOHYD 54 FOTENTIAL.

CARBOHYD 89 89 POTENTIAL.

CARBOHYD 89 89 POTENTIAL.

CARBOHYD 89 89 CC402395 CRC32;

SEQUENCE 186 AA; 21351 MW; CC402395 CRC32;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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P04545;
104545;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MATRIX GLYCOPROTEIN M2 (ENVELOPE-ASSOCIATED 2
                                                                                                                                                                                                                                                                                                                SEQUENCE
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01-APR-1993 (Rel.
01-APR-1993 (Rel.
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                                                        ELANGO N., SATAKE M., VENKATESAN S., "mRNA sequence of three respiratory two nonstructural proteins and a 22 J. Virol. 55:101-110(1985).
                                                                                                                                                           Human respiratory syncytial virus (strain A2).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
               SEQUENCE FROM N.A. MEDLINE; 85135082.
                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 85237684.
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                                                                         K structural protein.";
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EMBL; U50362; AAB86675.1; ...
EMBL; U50363; AAB86677.1; ...
EMBL; U603644; AAC55971.1; ...
PIR; A04034; WMNZZ2.
PIR; A04034; WMNZZ2.
Matrix protein; Envelope protein atrix protein 89 89 PO CARBOHYD 99 89 PO CARBOHYD 191 191 PO'S EQUENCE 194 AA; 22154 MW; ...
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Q84132;
15-Jrr
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J. Virol. 54:65-71(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 95266253.

CONNORS M., CROWE J.E. JR., FIRESTONE C.Y., MURPHY B.R., COLLINS P.L.;

CONNORS M., CROWE J.E. JR., FIRESTONE C.Y., MURPHY B.R., COLLINS P.L.;

"A cold-passaged, attenuated strain of human respiratory syncytial

virus contains mutations in the F and L genes.";

virology 208:478-484(1995).
                                                                                  SEQUENCE FROM N.A.

MEDLINE; 95088607.

ALANSARI H.M., POTGIETER L.N.D.;

*Molecular cloning and sequence analysis
nucleocapsid protein, matrix protein and
ovine respiratory syncytial virus.";

J. Gen. Virol. 75:3597-3601(1944)...
                                                                                                                                                                                                                                                                                                              Ovine respiratory syncytial virus (strain WSU 83-1578) (
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
[1]
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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of the phosphoprotein, 22K (M2) protein of the

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A_SEQUENCE 1.0
VMEM_LVX
P27331;
01-AUG-1992 (1
01-OCT-1994 (1)
HYPOTHETICAL 1
Lily virus X.
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Transmembrane.
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72
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CARBOHYD 54 54 POTENTIAL
CARBOHYD 89 89 POTENTIAL.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
[1]
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01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
11.4 KD MEMBRANE PROTEIN (ORF 3).
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PF01307; Plant_vir_prot; 1.
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            23, Created)
23, Last sequence up
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KD PROTEIN (ORF 3).
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POTENTIAL.
; CFA2CE4A CRC32;
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VMEM_LVX
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TRANSMEM 77
TRANSMEM 77
SEQUENCE 108
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MEDILINE; 90218039.

MEMELINE; 9.218039.

MEMELINE; 9.218039.

DERKS A.F.L.M., ASJES C.J., BOL J.F.;

DERKS A.F.L.M., ASJES C.J., BOL J.F.;

"Homologies between the genomes of a carlavirus (lily symptomless virus) and a potexvirus (lily virus X) from lily plants.";

J. Gen. Virol. 71:917-924(1990).

J. Gen. Virol. 71:917-924(1990).

J. SIMILARITY: TO ORF3 PROTEIN FROM OTHER POTEXVIRUSES AND TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                           the European Bioinformatics Institute. There are no resture by non-profit institutions as ion as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                   sequences.";
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01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
12 KD MEMBRANE PROTEIN (ORF 3).
Potato virus M (Strain Russian) (PVM).
Viruses; SSRNA positive-strand viruses, no DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1.0
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EMBL; D14449; BAA03341.1; EMBL; X53062; CAA37234.1; PIR; PN0003; WMVYP2.
                                                                                                                                                                                                                                                                                                                                                               RUPASOV V.V., MOROZOV S.Y., KANYUKA K.V., ZAVRIEV S.K.; "Partial nucleotide sequence of potato virus M RNA shows similarities to protexviruses in gene arrangement and the encoded amino acid
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89293091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 VLCHTTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEM_PVMR
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72
108 AA;
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POTENTIAL.
6E8DFF03 CRC32;
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Р07579:
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VSDA OR SPVR.
Salmonella du
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TRANSMEM
SEQUENCE
 SEQUENCE FR
MEDLINE; 91
KRAUSE M.,
"Molecular
                                                                                               01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
VIRGLENCE GENES TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                               EMBL; M12921;
PIR; A23368; V
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         MCGRAW T., MINDICH L., FRAN "Nucleotide sequence of the bacteriophage phi 6: novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage phi-6.
Viruses; dsRNA viruses;
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01-APR-1988 (Rel.
01-JAN-1990 (Rel.
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PIR; ;
PFAM;
                                                           Plasmid pSDL2.
Bacteria; Proteobacteria;
                                                                                                                                                            SEQUENCE 1.0
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J. Virol. 58:142-151(1986).
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                                                   Salmonella.
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C54333; C54333.
; PF(01307; Plant_vir_prot;
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E FROM N.A.
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M., ROUDIER C., I
lar analysis of 1
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73
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93
11907
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f the small double-stranded RNA segment of ovel mechanism of natural translational
 FIERER J., HARWOOD J.,
the virulence locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cystoviridae;
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                                                            subdivision;
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                                                            Enterobacteriaceae;
 GUINEY D.;
the Salmonella dublin
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IIAA_SEQUENCE 1.0
ID VRPR_SALTY
AC P13041;
DT 01-JAN-1990 (F
DE VIRULENCE GENER
GN MKAC OR SPVR (O
Bacteria; Prot
OC Bacteria; Prot
OC Bacteria; Prot
OC Salmonella.
RN [1]
RA PULLINGER G.D.
RT "NUCLEOTIDE SE
RN SEQUENCE FROM
RX MEDLINE; 90016
RA PULLINE; 9006
RA MEDLINE; 9006
RA MEDLINE; 9006
RA TAIRA S., RHEN
RA TAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-1275 WILD TYPE;
MEDLINE: 90016881.
MEDLINE: 90016881.
MILLIAMSON (
MILLIAMSON
SEQUENCE FROM N.A.
MEDLINE; 92041614.
CALDWEEL A.L., GULIG F.A.;
The Salmonella typhimurium virulence plasmid regulator of a plasmid-encoded virulence gene.
J. Bacteriol. 173:7176-7185(1991).
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MO1. Microbiol. 5:307-316(1991).

11- FUNCTION: POSITIVE REGULATOR FOR THE PLASMID-ENCODED VIRU
FACTORS SPVA, SPVB, AND SPVC.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SUBCELLULAR LOCATION CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 90060335.

TAIRA S., RHEN M.;

"MOLECULAr organization of genes constituting the viru
determinant on the Salmonella typhimurium 96 kilobase
FEBS Lett. 257:274-278(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last segue
15-DEC-1998 (Rel. 37, Last annot
VIRULENCE GENES TRANSCRIPTIONAL
MKAC OR SPVR OR VAGA.
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PROSITE; P500044; HTH_LYSR_FAMILY; 1.

PFAM; PF00126; HTH_L; 1.

PFAM; PF00126; HTH_L; 1.

PFAMING; Virulence; Transcription region, BIND 21 40

EDUA_BIND 21 40

SEQUENCE 297 AA; 33849 MW; DA84449
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    Created Activator.

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40 H-T-H MOTIF (POTENTIAL).
33849 MW; DA84490B CRC32;
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IIAA_SEQUENCE 1.0

ID WN11_CHICK
AC P49339;
DT 01-FEB-1996 (F
DT 01-FEB-1996 (F
DT 01-FEB-1996 (F
DT 01-FEB-1996 (F
DT 01-GT-1996 (F
DT 01-GT-1996 (F
DT 01-GT-1996 (F
DT 01-FEB-1996 (F
RA FANDA N. OHUT
RT "A Chicken Wn1
RL Biochem. Bioph
RN [2]
RP SEQUENCE FROM
RX MEDLINE; 96066;
RA TANDA N. KAW
RT "Cloning and o
RT embryo.";
RL DNA Seq. 5:27;
CC -:- FUNCTION:
CC -:- FUNCTION:
CC -:- SUBCELLULY
CC -:- SUBCELLULY
CC -:- TISSUE SPI
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MEDILINE; 91244158.

TAIRA S., BAUMANN M., RIIKONEN P., SUKUPOLVI S., RHEN M.;

TAIRA S., BAUMANN M., RIIKONEN P., SUKUPOLVI S., RHEN M.;

TAIRA S., BAUMANN M., RIIKONEN P., SUKUPOLVI S., RHEN M.;

TAMINO-terminal sequence analysis of four plasmid-encoded virulence associated proteins of Salmonella typhimurium.";

FEMS Microbiol. Lett. 61:319-323(1991).

-I- FUNCTION: POSITIVE REGULATOR FOR THE PLASMID-ENCODED VIRULENCE FACTORS SPVA, SPVB, AND SPVC.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC.

-I- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid;
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                         P49339;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
WNT-11 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X16111; CAA34244.1; -. PIR; S06089; S06089. PIR; S06670; S06670.
                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken)
Eukaryota; Metazoa; Cho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 95298011.
TANDA N., OHUCHI H.,
"A chicken Wnt gene,
                                                                                                                                                                                                                                                                                                                                                                                             WNT11 OR WNT-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00044; HTH_LYSR_FAMILY; PFAM; PF00126; HTH_1; 1
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 96063018.
TANDA N., KAWAKAMI Y., SAITO T.,
"Cloning and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5,2
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                                                                                            Seq. 5:277
DIAMETERS.
SUBCELLULAR LOCATION: POSSIBLY
EXTRACELLULAR MATRIX.
TISSUE SPECIFICITY: EXPRESSED
                                                                                BOTH LIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSTDHALHI KGVALCTSLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDFLINKKLK IFITLMETGS
                                                            ", 5:277-281(1995).
NCTION: MAY PLAY A ROLE IN
TH LIMB AND FEATHER BUDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 297
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                                                                                                                                                                                                                                     Biophys.
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297 AA;
                                                                                                                                                                                                                                                                                                                                           Galliformes;
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                                                                                                                                                                                                                                     Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 14, 2000 08:03
                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Archosauria; Aves; mes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                     YOSHIOKA H., NOJI S., NOHNO T
Wnt-11, is involved in dermal
s. Commun. 211:123-129(1995).
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                                                                              IN THE FORMATION OF DERMAL STRUCTURE.
S. IS LIKELY TO SIGNAL OVER ONLY FEW (
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Wnt-4 and
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                                              SECRETED AND
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              DERMATOME
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                                            ASSOCIATES WITH
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                                                                                CELL
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GYRWGGCADN

FSDAPMKMKK AISHTIARAC

KTCWKGLQEL

LLDLERGTRE LVVSQVQLCR MKPSPQFFLA

51 Н

AFLSLILQTG ICYGIKWIAL

QAAREVIKTC

RKTFSDMRWN

SKTPSSLALN QTQHCKQLEG

251 201

PMGTRKYLVP LKASLEMKCK

KDIDIRPVKE CHGVSGSCSI LNYGLIMGSK SAFVYALSAA SNLELMOTII

DECMKNEKVG RDIALDLKNK SGSQANKLMH TTGDLPGCSC

LMCCGRGYNP

YMDKVVERCH TELIYLOSSP

CKKCERTVER SHGTQDRQCN YLSATKVVHR LHNSEVGRQV GPIPGETPGP

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WN11_CHICK Length:
                                                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                            PFAM;
                                                                                                                                                                                                                                                                                                                                        D31901; BAA06699.1; -. TE; PS00246; WNT1; 1. PF00110; wnt; 1.
                                       354 February 14, 2000 08:03
                                           354
40
90
300
300
304
39507
                                                                                                                                 Glycoprotein; Signature of the control of the contr
                                                                      MW:
                                                                      POTENTIAL.
; 14039075 CRC32;
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       Type: P
       Check: 4630
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IIAA_SEQUENCE 1.0

ID WN11_COTJA STANDARD; PRT; 354 AA.

AC P51891;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 10-JUL-1998 (Rel. 36, Last annotation update)
DT 10-JUL-1998 (Rel. 36, Last annotation update)
DT 10-JUL-1998 (Rel. 36, Last annotation update)
DC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Arcio CRI Last annotation (Japanese quail)
CC Eukaryota; Metazoa; Chordata; Craniata; Arcio Coturnix (Japanese; Phasianinae; Coturnix Noturnix (Japanese quail)
CC TISSUE-MESCOREM;
CC TISSUE-MESC 351 301 YVCK KTSNGSDSCD CKYHWCCYVT Archosauria;

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WN11_HUMAN STANDARD; PRT; 354 AA.

O95014;

15-JUL-1999 (Rel. 38, Created)

15-JUL-1999 (Rel. 38, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

MNT-11 PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEAM; PENULLY WILL, I. Developmental protein; Glycoprotein; Signal.

SIGNAL 24 POTENTIAL.
CCHAIN 25 354 WNT-11 PROTEIN.
CARBOHYD 40 POTENTIAL.
CARBOHYD 90 POTENTIAL.
CARBOHYD 300 90 POTENTIAL.
CARBOHYD 300 POTENTIAL.
CARBOHYD 304 304 POTENTIAL.
SEQUENCE 354 AA; 39457 MW; 3FC9C358 CRC32;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE; 98434463.

LAKO M., STRANCHAN T., BULLEN P., WILSON D.I., ROBSON S.C., LINDSAY S.;

"Isolation, characterisation and embryonic expression of WNT11, a gene
which maps to 11q13.5 and has possible roles in the development of
skeleton, kidney and lung.";

Gene 219:101-110(1998).

11- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.

11- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (see http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
EMBL; Y13843; CAA74159.1;
EMBL; Y13844; CAA74159.1;
EMBL; Y13845; CAA74159.1;
EMBL; Y13846; CAA77159.1;
EMBL; Y13847; CAA74159.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00110; wnt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                                                                                                   EXTRACELLULAR MATRIX.
SIMILARITY: BELONGS TO THE WNT FAMILY.
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WN11_HUMAN Length: 354
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SEQUENCE
                                                                                                                                                                                                             CHRISTIANSEN J.H., DENNIS C.L., WICKING C.A., MONKLEY S.J.,
WILKINSON D.G., WAINWRIGHT B.J.;
WAIKINSON D.G., WAINWRIGHT B.J.;
Warine Wart-11 and Wart-12 have temporally and spatially restricted
expression patterns during embryonic development.";
Mech. Dev. 51:341-350(1955).

I.FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMFERS.
I.FUNCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXPRACELLULAR LOCATION:
DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.
I. DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _SEQUENCE 1.0

wN11_MOUSE STANDARD; PRT; 354 AA.

P48615;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

WNT-11 PROTEIN PRECURSOR.

WNT11 OR WNT-11.
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; X70800; CAA50070.1; -.
MGD; MGI:101948; WNTI1.1.
PROSITE; PS00246; WNTI; 1.
PERAM; PP00110; Wnt; 1.
Developmental protein; Glycoprotein; Signal SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MIM; 603699; -.
PROSITE; PS00246; WNT1; 1
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WN11_MOUSE Length: 354 February 14, 2000 08:03 Type: P Check:
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WNT4_DROME
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SEQUENCE
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SEQUENCE FROM N.A.

MEDILINE; 95171909.

GRABA Y., GIESELER K., ARAGNOL D., LAURENTI P., MARIOL M.-C.,

BERENGER H., SAGNIER T., PRADEL J.;

"DWnt-4, a novel Drosophila Wnt gene acts downstream of homeotic complex genes in the visceral mesoderm.";

Development 121:209-218(1995).

1- FUNCTION: ACTS DOWNSTREAM OF HOMEOTIC COMPLEX GENES IN THE VISCERAL MESODERM AND IS REQUIRED FOR EMBRYONIC SEGMENTATION.

1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA0589;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
WNT-4 PROTEIN PRECURSOR (DWNT-4).
                                                                        CARBOHYD
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                                                                                                                                                                                             EMBL; L25316; AAA67470.1; -.
FLYBASE; FB9N0010453; Wnt4.
PROSITE; PS00246; WNT1; 1.
PFAM; PF00110; Wnt; 1.
                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                    Developmental
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AC 010280;
DT 01-NOV-1997 (I
DT 01-NOV-197 (I
DT 01-NOV
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 36, Last annotation update)
12-NOV-1997 (Rel. 37, KD PROTEIN (ORF19).
13-YEVEN AND VIEWS (ORF19).
14-YEVEN AND VIEWS (ORFN).
15-YEVEN AND VIEWS (ORNA STAGE).
15-YEVEN AND VIEWS (ORNA STAGE).
15-YEVEN AND VIEWS (ORNA STAGE).
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                            EMBL; U75930; AAC59018.1; -. Hypothetical protein. SEQUENCE 298 AA; 34666 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
-i- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AHRENS C.H., RUSSELL R.R., FUNK C.J., ROHRMANN G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 97271300.
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protein.
38 AA; 34666 MW; 9D51A0D9 CRC32;
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo [1] Q15053; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) HYPOTHETICAL PROTEIN KIAA0040. SEQUENCE 1.0 151 251 201 101 51 <u>سر</u> DANAIRTDLN MAGSCWLLFV VFQPQIHKNG SWILSARRAR IVMHCWNMYV INLSHLAAFL MLVQVNYFLQ LVLHAALFGL CSFAFVFALM ATVTARYAFL LELEDSAHSI STANDARD; NRPHNYFPFC QQKETRRKPN CVYYDNEMKK LGPYVLATIT RARNITUTLL METEKEYDTA CVGCRMEVRH HVPVLDALIR HHDRQSLCWS GVVVQEYEVH WAMYKMLLCY ROTGOTONVS 153 KGLEMRSNFY RLIFQHKRRA DEPTVFNQNQ Ą MKTVVALAHL EEEEHESNMR GALTMLALLA

Y021_NPVOP Length: 298 February 14, 2000 08:03

Type: P Check:

562

MGSHPHGHAL AGLAKLGIIV

AGGQGLPGNL GYGGTMLNGG GYGGAAGMGI

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Y040_HUMAN Length: 153
                                                                                                                                                                                          STRAIN-ATCC 33530 / G-37;

MEDLINE; 96026346

FRASER C.M., GOCAVNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A., FRASER C.M., GOCAVNE J.D., WHITE O., ADAMS M.D., CLAYTON G., KELLEY J. FLEISCHMANN R.D., BUIT C.J., KERLAVAGE A.R., SUTTON G., KELLEY J. FLEICHMAN J.E., WEIDMAN J.E., SAMLL K.V., SANDUSKY M., FURRMANN PRITCHMAN J.E., SAUDEK D.M., PHILLIPS C.A., MERRICK TOMB J.-F., DOUGHERTY B.A., BOTT K.F., HU P.-C., LUCIER T.S., PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996
01-FEB-1996
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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SATO S., NAGASE T., SEKI N., ISHIKAWA K.-I., TABATA S.;
"Prediction of the coding sequences of unidentified human genes. I.
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                  SEQUENCE OF 125-243 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 94075230.
PETERSON S.N., HU P.-C., BOTT K.F., HUT
"A survey of the Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up.
15-DEC-1998 (Rel. 37, Last annotation HYPOTHETICAL PROTEIN MG209.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE; 96026346.
                                                                                    sequencing.
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                                                quencing.";
Bacteriol. 175:7918-7930(1993).
- SIMILARITY: BELONGS TO THE RLU
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                                          FAMILY OF PSEUDOURIDINE SYNTHASES
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by using
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TON G., KELLEY J.M.,
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Y209_MYCGE
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EMBL; U02214; AAD12509.1; -.
TIGR; MG209; -.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
HYPOTHETICAL PROTEIN MG209 HOMOLOG.
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                        EMBL; AE000053; AAB96191.1; PROSITE; PS01129; PSI_RLU; 1 PFAM; PF00849; YABO; 1. PFAM; PF01479; S4; 1.
                                                                                                                                                                                                                                                                                               STRAIN-ATCC 29342
MEDLINE; 97105885
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
SEQUENCE 3
                                                                                                                                                                                                                                          pneumoniae."
                                                                                                                                                                                                                                                                    HERRMANN R.;
                                                                                                                                                                                                                                                                                                                                                    Mycoplasmataceae;
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                                                                                                                                                                                                                                                      Complete sequence analysis of the genome
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                                                                                                                                                                                                          leic acids Res. 24:4420-4449(1996).
SIMILARITY: BELONGS TO THE RLU FAMILY OF PSEUDOURIDINE SYNTHASES.
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308 AA; 34996 MW;
              protein
AΑ;
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 35228 MW;
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3375E3F5 CRC32;
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Y209_MYCPN

Length: 309

February 14, 2000 08:03

Type: P

QRLDTFLATL

LNLSRVKVAK LIVDGLVSVN

GKKITKNGWL

51

VQPEDRVHVN WSEELFEKVP VEVQPYDFPL DILYEDEQIM VVNKPNGLIS

HPTSFNESES LLGAALFHCN HQPVFLVHRL DRDTSGVIML AKNQSSLLHI

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SO THE REAL PROCESS OF THE
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15-JUL-1999
15-JUL-1999
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
HYPOTHETICAL PROTEIN MG280.
                                                     HYPOTHETICAL TP0373.
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TIGR; MG280; -.
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STRAIN-ATCC 33530 / G-37;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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TRANSMEM
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                            reponema
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pallidum.
Spirochaetales;
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265 AA;
                                                                         (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
L PROTEIN TP0373.
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29566 MW;
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     Spirochaetaceae;
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Y373_TREPA Length: 477 February 14,
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SEQUENCE FROM N.A.
STRAIN-NICHOLS;
MEDLINE; 98332770.
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P75172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALLBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAGN
HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
PROBABLE RNA HELICASE MG425 HOMOLOG.
MYCOPlasma pneumoniae.
Bacteria; Firmictes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                            451
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                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE; 97105885.
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 This SWISS-PROT entry is cop-
between the Swiss Institute
                                          "Complete sequence
pneumoniae.";
Nucleic Acids Res.
-!- SIMILARITY: TO
                                                                                                              HIMMELREICH R.,
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                                                                                                  HERRMANN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ence 281:375-388(1998).
SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY
                                         SIMILARITY:
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                           24:4420-4449(1996).
OTHER "DEAD" BOX FAMILY HELICASES.
                                                                                   analysis of the genome of the bacterium Mycoplasma
 is copyright. It is produced through a collaboration - stitute of Bioinformatics and the EMBL outstation -
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Y464_MYCGE
Y464_MYCGE
947702;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence updated)
1 01-0CT-1996 (Rel. 34, Last annotation up
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FFAM; PF00270; DEAD; 1.
FFAM; PF00271; helicase_C; 1.
Hypothetical protein; Helicase; ATP -binding; RNA-binding.
HP_BIND 47 54 DEVD BOX.
SITE 154 157 DEVD BOX.
SEQUENCE 450 AA; 51244 MW; 4D9D6B21 CRC32;
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or send an
                                                                                                                                                                                                           FRASER C.M., GOCAYNE J.D., WHITE O., ADAMS M.D., CLAYTON R.A., FLEISCHMANN R.D., BUJT C.J., KELLAYJGE E.R., SUTTON G., KELLEY J.M., FRITCHMAN J.L., WEIDMAN J.F., SMALL K.V., SANDUSKY M., FUHMANN J.L., METIDMAN J.F., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M., FUNDER D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M., PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C., "The minimal gene complement of Mycoplasma genitalium.", Science 270:397 403(1955).

SCIENCE 270:397 403(1955).

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 96026346.
FRASER C.M., GOCAYNE J.D.
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                              EMBL; U39728; AAC72484.1; EMBL; U39733; AAB01654.1; TIGR; MG464; -.
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Transmembrane.
9 POTENTIAL
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MBL outstation -
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TLAYGPFYGW CTQTLAQPWT

FVWPASQIVL

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EIGYNFGTTG PIMYATRVPL

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LKNLKKAWGI

IFLTIVGLWG

MPLNLNKKHK ELKTTFNPFW

ILSLIVLLFL VRLITIVITL NSTLALEKMN EVQGKLAEIN AKYKGALDLQ

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Y464_MYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN MG464 HONOLOG.
MYCOPLASMa pneumonlae.
MScoplasma pneumonlae.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-- SIMILARITY: TO A M.CAPRICOLUM HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae."; % \left( 1\right) =\left( 1\right) ^{2}
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                                                                                                                                                                                                                                EMBL: AE000017;
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February 14, 2000 08:03
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                                                        CRC32;
Type:
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                                                                                                P55661;
01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsib.ch).
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                                                                                                                                                YATG_RHISN
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HSSP; P14061; IPDV.
PROSITE; PS00061; ADH_SHORT; 1.
PFAM; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular basis of symbiosis between Rhizoblum and legumes.";
Nature 387:394-401(1997).
-i- SIMILARIY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
FAMILY (SDR). STRONG, TO BACTERIAL 'YDFG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE Y4EK
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                                Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alph
                                                                                                                                                                                                                                                                                                                                      Hypothetical protein;
NP_BIND 8 3
ACT_SITE 147 14
SEQUENCE 248 AA; 2
                                                                                 01.NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
PROBABLE AMINO-ACID ABC TRANSPORTER PERMEAS
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SEQUENCE FROM N.A
                       Rhizobiaceae;
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1FDV.
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                                                                                                                                                  STANDARD;
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NAD OR NADP (BY SIMILARITY).

S SIMILARITY.

6679 MW; A7C5BF45 CRC32;
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                                    Rhizobiaceae
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TRANSMEM 32
TRANSMEM 64
TRANSMEM 166
TRANSMEM 166
TRANSMEM 161
TRANSMEM 166
SEQUENCE 231 AA;
                                                           SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067:

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., REICH C.I.,

SUTTON G.G., BLAKE J.A., FITZEBRALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEINSTOKK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., FRASER C.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 057926;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
putative 2-isopropylMalate/HOMOCITRATE SYNTHASE MJ0503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97305956.

FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSEN PERREIT X.;

"MOLECULAR basis of symbiosis between Rhizobium and legumes "MOLECULAR BASIS OF SYMBIOSIS BETWEEN RHIZOBIUM ADDING-PROTEIN-DEPENDENT SYSTEM Y4TEFCH FOR AN ANINO ACID. PROBABLY RESPONSIBLE TRANSLOCATION OF THE SUBSTRAIL ACROSS THE MEMBRANE.

"IS SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
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jannaschii.";
Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii
Archaea; Euryarchaeota; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lethanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE 1.0
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M; PF00528; BPD_transp; 1.
othetical protein; Transport; Amino-acid transporter membrane; Plasmid.
MINEREM 9 29 POTENTIAL.
NINEM 32 52 POTENTIAL.
NINEM 84 POTENTIAL.
NINEM 86 106 POTENTIAL.
NINEM 161 181 POTENTIAL.
NINEM 161 181 POTENTIAL.
NINEM 196 216 POTENTIAL.
NINEM 196 216 POTENTIAL.
NINEM 196 216 POTENTIAL.
NINEM 196 216 POTENTIAL.
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SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE HISMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGGIYLILTI VASALVRIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALALGIQYSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLVSIMKDVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AWPAAVLIEF
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETHVILPQA
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FOR THE
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Y503_METJA Length: 406
                                                                                                                                            STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE; 96337999.

BUIT C.J., WHITE O., OLSEN G.J., ZHOU L., ELEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEER R., KIRKNESS E.F., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAIME B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus

Jannaschii.";

Science 273:1058-1073(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P81311;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN MJ0703.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
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Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67500; AAB98494.1; -. TIGR; MJ0503; -.
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                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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06 AA; 45364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGIDYDREML CEIVKKVKEI REEGKFITDE
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Y788_BORBU

Length:

440

February 14,

2000

08:03

Type:

ש

1619

SGGADSTALL LNLKYYLSNN

251

YSFDLKTFLD FPKYLVFRLI FKILNSEGIA AKVSYKALNE AFKVEINRKI

NIALQIKKCD AHNENDQIET SLNNIGFFVD EFADYFGKDE

101 151

NRNIIRPLLE

LDKNRVIVAF
EHVKGFCDLY
KENGANYIAL
VSRLEIENFL

IIMRFFQGSF STNAQNLYLR

51

MHFLDENIQI KIDKFYKKNS

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SECOND DESCRIPTION OF THE PROPERTY OF THE PROP
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TIGR; MJ0703.1; -
Hypothetical protein; Trans
TRANSMEM 14 34
TRANSMEM 35 55
TRANSMEM 76 96
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 98065943.

MEDLINE; 98065943.

FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A., DEFRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A., GWINN M. LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M. DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D., HANSON M., PETERSON J., KERLAYAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., VAN TUGT R., PALMER N., ADAMS M.D., GOCAYRE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;

"Genomic sequence of a Lyme disease spirochaete, Borrelia ""Genomic sequence of a Lyme disease spirochaete, Borrelia
Hypothetica.
SEQUENCE '
                                                                                                                                                                                                                                                                                                                                                                                                         burgdorferi.";
Nature 390:580-586(1997).
-i- SIMILARITY: BELONGS TO THE UPF0072 (MESJ/YCF62) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
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STRAIN-ATCC 35210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y788_BORBU
051728;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence u.
15-JUL-1999 (Rel. 38, Last annotation
MYPOTHETICAL PROTEIN BB0788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
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                                                                    AE001177; AAC67121.1; -. BB0788; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
al protein.
440 AA; 51471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 AA;
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14 34 POTENTIAL.

35 55 POTENTIAL.

76 96 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e disease spirochete).
Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKPIITIVGI VISAVAFTIS ILWGMLFLIL
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; 2336A893 CRC32;
   DF4B6E4A CRC32;
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NNVLLKTNDF

FLEKRHNKIN LIFKRDEKFY KPFDFILEVG

KWHSLSLGKI

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ROCCORDITATION
                                                                                                                                                                                                                                                                                                                                                                     Y79B_METJA Length: 170
IAA_SEQUENCE 1.0

Y953_MYCTU STANDARD; PRT; 282 AA.

C P71557;

O1-NOV-1997 (Rel. 35, Created)

T 15-DEC-1999 (Rel. 35, Last sequence update)

T 15-DEC-1999 (Rel. 39, Last annotation update)

E HYPOTHETICAL 30.9 KD PROTEIN RV0953C.

N RV0953C OR MTCY10D7.21.

S Mycobacterium tuberculosis.

S Mycobacterium tuberculosis.

S Mycobacterium tuberculosis.

Actinomycetales; Corynebacterineae; Mycobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Myco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43057;
MEDLINE; 96337999.
BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOCHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KALINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOLES C.R., VENTER J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
landsschil":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
HYPOTHETICAL PROTEIN MJ0795.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67524; AAB98801.1; -. TIGR; MJ0795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
TRANSMEM
                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SIMILARITY: TO MJ1249.1, MJ0210.1 AND MJ0785.1.
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                                                                                                                                                                                                                                                                 AVLFFIFIVA
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                                                                                                                                                                                                                                                                                                                                                                                                       31
91
170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       protein; Transmembrane.
6 26 POTENTIAL.
31 51 POTENTIAL.
91 111 POTENTIAL.
70 AA; 19689 MW; OBF2A40D CRC32;
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                                                                                                                                                                                                                                                                 FTISEFYKTY
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                                                                                                                                                                                                                                                                                                                                                                     February 14, 2000 08:03 Type:
                                                                                                                                                                                                                                                                 RIRIYEKGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                   IEGIAFYSWE
                                                                                                                                                                                                                                                                                                                                     LLFILLAFGS LVGITLILIY
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                                                                                                                                                                                                                                                                                                   IYFSGTFYNS
                         Mycobacterium.
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II AA_SEQUENCE 1.0
II 7988_METJA
AC Q58395;
DT 15-JUL-1998 (I
RA COTTON G-G., I
RA COTTON M.D.,

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X A COLE S.T., BROSKH C., GAS S., BARRY C.E. III, TEKALA F., RA GONDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKALA F., RA GONDON S.V., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., PELLWELL T., GENTLES S., HAMLIN N., HOLROYD S., RA HORNSPY T., JAGELS K., KROGH A., MCLEAN J., MUTEN S., MURPHY L., RAJANDREAM M.A., ROSERS J., RA RUTTER S., SEBGER K., KROGH A., RAJANDREAM M.A., ROSERS J., RA RUTTER S., SEBGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E. RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;

RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;

RI "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence";

RI Nature 393:537-544(1998).

RL Nature 393:537-544(1998).

RL Nature 393:537-544(1998).

RL Nature 393:537-544(1998).
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                                                                                                                              RC STRAINJAL-1 / DSM 2661 / ATCC 43067;

RX MEDLINE; 96337999.

RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

RA OVERBEER R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

RA SCOTT J.L., GEOGHAGEN N.S.M., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., BONDOVSKY M.,

RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BONDOVSKY M.,

RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,

RT Jannaschil.*;

Science 273:1058-1073(1996).

CC --- SIMILARITY: SOME, TO M.JANNASCHII MJ1633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q58395;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
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!!AA_SEQUENCE 1.0
ID YABP_ECOLI
AC P39220; P75632
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YABP_ECOLI STA
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01-FEB-1995 (Rel.
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MEDLINE; 90108714.
KATO J., CHU L., KITANO K., DEVAULT J.D., KIMBARA K.,
CHAKRABARTY A.M., MISRA T.K.;
CHAKRABARTY A.M., MISRA T.K.;
synthesis in Pseudomonas aeruginosa: characterization of the algR2
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
11-MAY-1991 (Rel. 18, Last annotation update)
13.0 KD PROTEIN IN ALGR3 3'REGION.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa.
Pseudomonas aeruginosa.
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PIR; JQ0150; JQ0150.
Hypothetical protein.
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MJ0988; -.
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01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
01-MAY-1992 (Rel. 22, Last annotation update)
HYPOTHETICAL 20.5 KD PROTEIN IN BCHF-CRTJ INTERGENIC REGION
RHOGODACTER capsulatus (Rhodopseudomonas capsulata).
Bacteria: Proteobacteria; alpha subdivision; Rhodobacter gro
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MEDLINE: 97426617

BLATTWER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V BLATTWER F.R., PLUNKETT G. III, BLOCH C.A., RODE C.K., MAYHEW G.F., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1.0
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MEDLINE; 93334977.
YURA T., WORI H., NAGAI H., NAGATA T., ISH
YURA T., MIZOBUCHI K., NAKATA A.;
"ISONO K., MIZOBUCHI K., NAKATA A.;
"Systematic sequencing of the Escherichia
the 0-2.4 min region.";
the 0-2.4 min region.";
Chicleic Acids Res. 20:3305-3308(1992).
                                                           BURKE D.H., ALBERTI M., ARMSTRONG G.A., HEARST J.E.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                SEQUENCE FROM N.A.
BURKE D.H., ALBERT
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EMBL; AE000116; AAC73167.1; -.
ECOGENE; EG12610; yabp.
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Unpublished observations (NOV-1994).
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IIAA_SEQUENCE 1.0
ID YBFT_BACSU
AC 031458;
DT 15-JUL-1998 (F
DT 15-JUL-1998 (F
DT 15-DEC-1998 (F
DE HYPOTHETICAL
GN YBFT
OC Bactillus Subtle
CC Bactillus Subtle
RT SEQUENCE FROM
RC STRAIN-168;
RT HAGA K., LIU I
RT SEQUENCE TAN
RC HAGA K., LIU I
RT SEQUENCE 100
RT STRAIN-168;
RT SEQUENCE 100
RT STRAIN-168;
RT SEQUENCE 100
RT STRAIN-169
RT SIBLIJET;
DR RSSP; P03118
RT ACT_SITE
SEQUENCE 24
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                                                                                                                                                                                                                                                                                                    YBFT_BACSU
                                                                                                                                                                                                                                                                                                                                                EMBL; AB006424; BAA33133.1; -.
EMBL; 299105; CAB12030.1; -.
HSSP; P09375; HOT.
SUBTILIST: BG12746; YBFT.
PROSITE: PS01161; GLCGBALMAC_ISOMERASE; 1
PFAM; PF01182; GluCGBALMAC_ISOMERASE; 1
PFAM; PS01161; GLUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-DEC-1998 (Rel. 3
HYPOTHETICAL 27.3 F
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                                                                                                                    101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAGA K., LIU H., YASUMOTO K., TAKAHASHI H., YOSHIKAWA H.;
"Sequence analysis of the 70kb region between 17 and 23 degree of the
Bacillus subtilis chromosome.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group.
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z11165; CAA77528.1; -. PIR; S17812; S17812.
201
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STRAIN=168;
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                                                                                                                                                                                                                                         MKILIAEHYE
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                                                                                                                                                                                                                                                                                                    Length: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
   MAEGPVTTDV PASILQKHNH
                                                                                                                    AACKVYEDLI
                                                                                                                                                                               VTTFNLDEYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36, Created)
36, Last sequence update)
37, Last annotation update)
KD PROTEIN IN GLTP-CWLJ INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             February 14, 2000
                                                                                                                                                                                                                                                                                                February 14, 2000
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                                                                                                                                                                               GLSPSHPQSY
                                                          GDPVLVPRLA
                                                                                                                    ROAGGIDVOI
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                                                                                                                                                                                                                                                                                                                                                           20883DBC CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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VTVIADYKAA QKLKSASFS
                                                                                                                 LGIGANGHIG
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                                                          ISMGIKTIME
                                                                                                                                                                                                                                                                                                                                                              CRC32;
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!!AA_SEQUENCE

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IPAA_SEQUENCE 1.0

ID TO21_METUA
AC Q586.18;
DT 01-NOV-1997 (I
DT 
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE: 96337999.

BULT C. J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., GCCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GCCAYNE J.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GCCCAYNE J.D., CERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBERK R., KIRKNESS E.F., WEINSTORK K.G., MEBRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCO8_KLEPN STANDARD; PRT; 373 AA.
(78454;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, East annotation update)
HYPOTHETICAL 42.6 KD PROTEIN IN CPS REGION (ORF8).
Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a copyreen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D21242; BAA04779.1; -.
PFAM; PFO0534; Glycos_transf_1; 1.
Hypothetical protein.
SEQUENCE 373 AA; 42641 MW; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
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virulent strain Chedid.";
J. Bacteriol. 177:1788-1796(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        responsible
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MEDLINE; 95204345
ARAKAWA Y., WACHAROTAYANKUN R., NAGATSUKA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation updat
L PROTEIN MJ1221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GITELSRILP NIYFLEDIQD
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synthesis
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jannaschii."; Science 273:1058-1073(1996) -!- SUBCELLULAR LOCATION: T

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus

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SO TITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YC21_METJA Length: 299
                                                                                                                                                                                                                                                                                                                                                                                           !!AA_SEQUENCE 1.0
ID YC38_PORPU
AC P51321;
                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
01-OCT-1996
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-AVONPORT;
REITH M.E., MUNHOLLAND J.;
"Complete nucleotide sequengenome.";
                                                                                                                                                                                                                                                                                                      Porphyra purpurea. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67563; AAB99234.1; -. TIGR; MJ1221; -.
                 EMBL; U38804; AAC08207.1; --
MENDEL; 10386; PORpu;ycf38;1
Chloroplast; Hypothetical pro
SEQUENCE 291 AA; 32427 MW
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TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                               YCF38
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL
                                                                                                                                                                                     Plant Mol. Biol. Rep. 13:333-335(1995).
-!- SIMILARITY: BELONGS TO THE YCF38 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pal protein; Transmembrane.
128 148 POTENTIAL.
177 197 POTENTIAL.
210 230 POTENTIAL.
236 256 POTENTIAL.
261 281 POTENTIAL.
                                                                                                                                                                                                                                                                                       Rhodophyta;
                                                                                                                                                                                                                                                                                                                                         (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 37, Last annotation update)
L 32.4 KD PROTEIN YCF38 (ORF291).
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197 PO
230 PO
256 PO
281 PO
32538 MW;
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                      stical protein.
32427 MW; 921437DB CRC32;
                                                                                                                                                                                                                         sequence of the Porphyra
                                                                                                                                                                                                                                                                                       Bangiophyceae; Bangiales;
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8E4A08F7 CRC32;
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                                                                                                                                                                                                                           purpurea chloroplast
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                                                                                                              !!AA_SEQUENCE 1.0
                                                                                                                                                                                                                                       YCBQ_ECOLI Length: 182
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                           P75991;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC
                                                                                                                                                                                                                                                                                         EMBL; AE000196; AAC74024.1; -... ECCGENE; EG13709; YCBC.
PFAM; PF00419; Fimbrial; 1.
Hypothetical protein; Fimbria;
Hypothetical protein; Fimbria;
SIGNAL
                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                  CGZ_ECOLI
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                                                                                                                                       DQTLTFKVDY IATGKATSGN VNAVTNFHIN
                                                                                                                                                              GTADTTQITA
                                                                                                                                                                                         ATKDSVVTLP
                                                                                                                                                                                                                                                                 25
182 AA;
                                                                                                  STANDARD;
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YC38_PORPU

Length:

291

February 14,

2000 08:03 Type:

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Check: 4681

Escherichia coli. Bacteria; Proteobacteria;

gamma

subdivision;

Enterobacteriaceae;

REGION

YCGZ.

FANQASSDAA THVALQMYMN DGTTAITPDT

PRT;

78 B DVSATKLQTN AFITVVCATS

GQVSGVQIDV PIELKDCDTT

VIKNATETEN

SVMAADDNAI

TDGSVTFNGK VIAPACTLVA

182

a; Signal.
 BYPOINTIAL.
 BYPOINTIAL FIMBRIAL-LIKE PROTEIN YCBQ.
 CE190E78 CRC32;

19025 MW;

February 14, 2000 08:03 Type: P Check:

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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
STRAIN-KIZ / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PODE C.K., MAYHEW G.F. RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F. GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MANU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
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15-JUL-1998 (Rel. 36, Last sen
15-JUL-1998 (Rel. 36, Last sen
HYPOTHETICAL FIMBRIAL-LIKE PRO
                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TESVIKISWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma subdivision;
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annotation updat
PROTEIN IN PEPN-
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IN PEPN-PYRD INTERGENIC REGION
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YCGZ_ECOLI Length: 78
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01-OCT-1996 (Rel. 34
01-NOV-1997 (Rel. 35
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-K12 / MG1555;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G
RILEY M., COLLADO-VIDES J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
BLATTMER F.R., PUUNKETT G. III, BLOCH C.A., PERNA N.T.
BLATTMER F.R., PUUNKETT G. GLASNER F.D., RODE C.K., N
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., N
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,
                                                                                                                                             AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H. KASHIMOTO K., KIMAKSANA M., KITAKAWA M., KITAKAWA M., MAKINO K., MASHIMOTO K., KIMAKSANA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., MASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAKEMOTO K., WADA C., YAMANOTO Y., YANO M., SUBMITTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical page 18 SEQUENCE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000215; AAC74248.1; -. ECOGENE; EG14288; YCgZ.
                                                                               MEDLINE; 90
CHA M.-K.,
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Science
                                                                                                                                                                                                                                                                                                               MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteok
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                                                                 "Thioredoxin-linked 'thiol peroxidase'
                                                                                                                       EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                      Biol. Chem.
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nce 277:1453-1474(1997).
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K.E.;
                                                                                                                                                                                                                                                                                     complete genome sequence 
are 277:1453-1474(1997).
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                                                                               96081923.
                                                                                                                       OF 221-262
                                                     la coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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                                         270:28635-28641(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAITRYFAK ANLHTQQETL GEIVTEILKD
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35,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8769 MW;
                                                                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Created)
. Last sequence update)
. Last annotation update)
PROTEIN IN TPX-FNR ITERGENIC REGION
                                                                                                                                                                                                                                                                                                                           T G. III, BLOCH C.A., PERNA N.T., BURLAND V S J., GLASNER F.D., RODE C.K., MAYHEW G.F., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                         subdivision;
                                                                                                                                                                                                                                                                                                    Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC32;
                                                                  from
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                                                                  periplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
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                                                                    space
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TOOOOO COOCE
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YCUZ_ECOLI
YCUZ_ECOLI
$TANDARD;
P77333; P76841;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                              AIBA H., BÁBA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMURA S., KITAGAMA M., KITAKAWA M., WAKINO K., MASHIMOTO K., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUDMILTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-K12 / MG165;
MEDLINE; 9742661'.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., P
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A.,
MAU B., SHAO Y.;
MAU B., SHAO Y.;
Science 277:1453-1474(1997).
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EMBL; D90771; CAB20835.1; -.
EMBL; D90770; CAB20825.1; -.
EMBL; U33213; -; NOT_ANNOTATED_CDS
ECOGENE; EG13906; ycji.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished observations (MAR-1996).
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MAYHEW G.F.
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YCQ5_YEAST Length: 317 February 14, 2000 08:03 Type: P Check:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1.0
                                                                                                                           101
                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 317 AA; 3
                                                                                                                                                                                                                                                                                 EMBL; X59720; CAA42332.1; -. PIR; S19425; S19425.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. HATAT D., JACQ C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 36.3 KD PROTEIN IN POL4-SRD1 INTERGENIC REGION
YCR01.5C OR YCR1.5C
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EMBL;
EMBL;
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PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
PFAM; PF00126; HTH_1; 1.
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VKSWDSLKDL
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                              INPQENPSKF
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IMQVTKM
                                                           LDKIDSGCNK
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                                                                                                                       QNHDDCLLRD
                            PKDKISSFEA DNGPAWLQFC
                                                         EGNSCSYWYI GDSETDLLSI LHPSTNGVLL
                                                                                          SHIFCNDLKK
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                            EKEGGKGAYI
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PRT;

131

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Length: 174

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2000

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Type: P

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8869

MTSQLEKEAR EWIEETLHTK LNAQLDLLDQ LQSGVILCRI CKEALGANIR

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YDM1_SCHPO
                                                  This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIRM-972;
GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.,
GENTLES S., CHURCHER C.M., EMBL/GenBank/DDBJ databases.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: TO YEAST YOR367W AND TO CALPONINS.
 Hypothetical SEQUENCE 1
                               EMBL; 298530; CAB11057.1; -.
                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
HYPOJUL-104 20.1 KD PROTEIN C4F8.10C IN CH
SPAC4F8.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 1.0
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SKELTON J., CHURCHER C.M., WOOD V., BARRELL B.G., RAJANDREAM SWEDMITTED (MAY-1997) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: TO M.JANNASCHII MJ0531.
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Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN C57A7.01 IN CHROMOSOME I (FRAGMENT).
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 174 AA; 2
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20141 MW;
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2DB8876B CRC32;
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IN CHROMOSOME I.
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15-JUL-1998 (Rel. 3
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15-JUL-1998 (Rel. 3
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01-FEB-1995
01-FEB-1995
15-JUL-1998
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Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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STRAIN-S288C / AB972;

DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO DIETRICH F.S., MULLIGAN J.T., CARPENTER J., CHEN E., CHERRY CHUNG E., BERNO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY CHUNG E., DUNCAN M., GUZMAN E., HARTZELL G., LEW H., LIN D., HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D., MOSEDALE D., NAKAHARA K., NAMATH A., NORGREN R., OEFNER P., OH PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN T., SMITH TAYLOR P., WEI Y., WEI Y., BUTTON M., BOTSTEIN D., DAVIS R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENTLES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 AA;
                                                                                                                                                                                                                           (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 36, Last annotation update)
L 14.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                            AB972;
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36, Last sequence up
36, Last annotation
KD PROTEIN C6B12.16
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                                                                                                                                                                Saccharomyces
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!!AA_SEQUENCE 1.0 ID YG29_BPSP1 AC P31653;

101 YDAREVFGDE

KAIWWQRAVA

VWPDYASYQT

KIDRQIPVFV

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YER4_YEAST
                                                                     YF58_MYCTU
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K COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HA COLE S.T., BROSCH R., GAS S., BARRY C.E. III, TEKAIA F., A GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., A BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., A BADCOCK K., DEVLIN K., FELTWELL T., GENLES S., HAMLIN N., HOLF HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY I.

A HORNSBY T., JAGELS K., FELTWELL T., GENLES S., SOARES R., SULST A CLIVER S., OSBORNE J., QUAIL M.A., RAJANNERAM M.A., ROGERS J., A RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULST TAYLOR K., WHITEHEAD S., BARRELL B.G.;

TAYLOR K., WHITEHEAD S., BARRELL B.G.;

TAYLOR K., WHITEHEAD S., BARRELL B.G.;

TOECIPHETING the biology of Mycobacterium tuberculosis from the complete genome sequence.";

I Nature 393:537-544(1998).

L Nature 393:537-544(1998).
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Q10772;
01-0CT-1996 (Rel. 34,
01-0CT-1996 (Rel. 34,
15-DE-1999 (Rel. 39,
HYPOTHETICAL 16.4 KD I
RV1558 OR MTCY48,07C.
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                                                                                                         Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                             EMBL; Z74020; CAA98333.1; -.
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  LRKTPLMRVE
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  HDGQYAIVAS
                                     PLDWSREQAD
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34, Last sequence up
39, Last annotation
KD PROTEIN RV1558.
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                                                                                                             16347 MW;
                                     TYMKSGGTEG
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    LGGAPKNPVW YHNVVKNPRV
                                                                                                             7F320812 CRC32;
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                                     TQLQGKPVIL
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                                        LTTVGAKTGK
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01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
HYPOTHETICAL 16.2 K
Bacteriophage SP01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAS YEAST P53138;
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STRAIN-WI;
MEDLINE; 93351562.
WILHELM K., RUEGER W.;
"Deoxyuridylate-hydroxymethylase of bacteriophage SPO1.";
Virology 189:640-646(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 97197974.
PAOLUZI S., MINENKOVA O., CASTAGNOLI L.;
"The genes encoding the transcription factor yTAFII60, the G4p1
protein and a putative glucose transporter are contained in a 12.3 kb
DNA fragment on the left arm of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 12.4 KD PROTEIN IN TAF60-G4P1 INTERGENIC REGION
YGL109W OR G3065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60728; CAA43135.1; -. PIR; S21504; S21504. Hypothetical protein.
                                                           EMBL; X97644; CAA66243.1; -. EMBL; Z72631; CAA96815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
                                                                                                                                                                                                                                   Yeast 13:85-91(1997).
                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetaceae;
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Length: 107
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                                  107 AA; 1
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                                  12435 MW;
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, Last sequence update)
, Last annotation update)
, Last annotation update)
PROTEIN IN GENE 29 5'REGION.
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                                  349DFDE6 CRC32;
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 08:03
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Type: P
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   Check:
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   6897
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YGLR_STRCO Length: 66 February 14, 2000 08:03 Type: P Check: 9954

502F47A4 CRC32;

51

DRVAQAMASR

RTDLIG

STANDARD;

PRT;

319

B

Н

MAKVTRDDVA RLAGTSTAVV

SYVINNGPRP VAPATRERVL AAIKELGYRP

P10941:
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUL-1999 (Rel. 33, Last annotation update)
HYPOTHETICAL PROTEIN 1 IN HYPOVIEULENCE-ASSOCIATED DS-RNA GENETIC
ELEMENT [CONTAINS: P29 PROTEINASE]

MAAQNPLADI QYYKRYKAKR RMEGQKKNSC TIAYIDSLQY YCRRSLSHKS

IIAA_SEQUENCE 1.0
IID YHA1_CRYPA
AC P10941;
DT 01-JUL-1989 (F
DT 01-JUL-1989 (F
DT 01-FEB-1996 (F
DE ELEMENT (CONT)
OS CATABLES; FU
DE CLYPHODECTIALES;
COMMANDE P103
OS PARASITICA; FU
OC DIAPOTITALES;
RN [1]
OC DIAPOTITALES;
RN [1]
OC STRAIN-EP713;
RX RAE B.P., HILL
RT "Characteriza
RT "Characteriza
RT With biologic
RT demains and 1
EMBO J. 8:657
CC THIS DS-R
CC THIS STAIN-EPT
CC THIS ST

SEQUENCE FROM N.A. STRAIN-EP713;

Diaporthales;

Fungi; Ascomycota; es; Valsaceae; Cryp

Cryphonectria

Cryphonectria parasitica

(Chesnut blight fungus) (Endothia

Euascomycetes; Pyrenomycetes

E CHESTNUT BLIGHT.

s associated of terminal

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a collaboration outstation

SIMILARITY: BELONGS TO

PEPTIDASE FAMILY C7

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!!AA_SEQUENCE 1.0
                                                                                                                                                                                                                     STRAIN-A3(2);
MEDLINE; 93345814.
WRAY L.V. JR., FISHER S.H.;
"The Streptomyces coelicolor glnR gene encodes a protein similar other bacterial response regulators.";
Gene 130:145-150(1993).
                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       005954;

01-FEB-1995 (Rel. 31, Last sequence up

01-FEB-1995 (Rel. 32, Last annotation

01-NOV-1995 (Rel. 32, Last annotation

HYPOTHETICAL PROTEIN IN GLNR 3'REGION

Streptomyces coelicolor.

Bacteria: Firmicutes; Actinobacteria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TLRPPLG
Hypothetical protein NON_TER 66 (SEQUENCE 66 AA; 7)
                                                                              EMBL;
                                                EMBL; L03213; AAA02839.1; -.
PIR; PN0644; PN0644.
HSSP; P15039; 1PRV.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
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 66
7094 MW;
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Streptomycetaceae; Streptomyces
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ion update)
ion (FRAGMENT).
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YHAl_CRYPA Length: 319 February 14, 2000 08:03 Type: P
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PIR; S03833; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haccillus subtilis.
Bacillus firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 33.7 KD PROTEIN IN CSPB-GLPP INT
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151
                           101
                                                                                                                                                                                                   EMBL; X96983; CAA65704.1; -.
EMBL; Z99108; CAB12749.1; -.
SUBTILIST; BG11598; YHCT.
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97124185.

NOBACK M.A., TERPSTRA P., HOLSAPPEL S., VENEMA G., B

"A 22 kb DNA sequence in the cspB-glpPFKD region at

Bacillus subtilis chromosome.";

Microbiology 142:3021-3026(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-168;
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                           IATHPNEDGQ
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PF00849; YA
                                                                                                              Length:
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                                                        GDRVFIDLQE
                           TGTLANLIAY
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                                                                                                                February 14,
                                                                                                                                               33740 MW;
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                           HYQINGETCK
                                                        SEASSVIPEY
                                                                                     LFSVLKTALK
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                           VRHVHRLDQD TSGAIVFAKH
                                                         GELDILFEDN
                                                                                      ASKPVIQDWM SHQQIKVNHE
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 KKGTINPPIG
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ID YHG3_YEAST
                                           !!AA_SEQUENCE 1.0
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HYPOTHETICAL 48.9 KD PROTEIN IN RPL14B-GPA1 II
YHR003C.
YHGN_ECOLI
P46851;
01-NOV-1995
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P38756;
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DU Z., FAVELLO A., FULTON L., GATTING S., GEISEL C., KIRSTEN J.,
KUCABA I., HILLIER L., JIER M., JOHNSTON L., ANGSTON Y.,
LATRRILLE P., LOUIS E.J., MACRI C., MARDIS E., MENEZES S., MOUSER L.,
NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
VAUDTN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C / AB972;
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S.,
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PIR; S46801; S46801
PFAM; PF00899; ThiF_family;
Hypothetical protein.
SEQUENCE 429 AA; 48883 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 265:2077-2082(1994).
-!- SIMILARITY: STRONG, TO YEAST YKL027W.
COFACTOR BIOSYNTHESIS PROTEIN A (MOAA)
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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32, Created
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YHGN_ECOLI
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EMBL; AE
ECOGENE;
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GOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BADDCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUALL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J. TAYLOR K., WHITEHEAD S., BARRELL B.G.;
                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence
15-DEC-1999 (Rel. 39, Last annotatio
HYPOTHETICAL 18.1 KD PROTEIN RV1829
RV1829 OR MTCY1A11.14C.
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                                                                               MEDLINE; 98295987.
COLE S.T., BROSCH
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STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; k
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15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e complete genome sequence of Escherichia coli K-12.";
ence 277:1453-1474(1997).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTE
SIMILARITY: BELONGS TO THE UPF0056 (MARC) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   U18997, AAA58232.1; -.
U18997, AAA58232.1; -.
AE0004201, AAC76459.1; -.
ENE, EG12941; YHGN.
ENE, EG12941; Transmembrane.
POTENTIAL.
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72 9
106 1:
139 1
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(Rel.
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37,
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, Last annotation update)
PROTEIN IN ASD-GNTU INTERGENIC
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           PEGWAFEYSR FQEAQKREIV EHSYLVAQAH QIVEQAHKVA LEASSSGRAA
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READUSCULTURE SERVICE 
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A COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARR GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., A GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., A DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLKOY A HORNSBY T., JAELS K., KROGH A., MCLEAN J., MOLHAMLIN N., HOLKOY A HORNSBY T., JAELS K., KROGH A., MCLEAN J., MOURE S., OSBORNE J., OUAIL M.A., RAJANDREAM M.A., ROGERS J., OLIVER S., OSBORNE J., OUAIL M.A., RAJANDREAM M.A., ROGERS J., A CLIVER S., SEEGEER K., SKELTON S., SQUARES S., SQARES R., SULSTON A TAYLOR K., WHITEHEAD S., BARRELL B.G.;

TOCOMPLETE GENOME SEQUENCE.";

TOCOMPLETE GENOME SEQUENCE.";

RECOMPLETE GENOME SEQUENCE
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      EMBL; 274025; CAA98390.1; --
PFAM; PF00582; USp; 2.
Hypothetical protein
SEQUENCE 317 AA; 33879 MW
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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STRAIN-H37RV;
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01-0CT-1996 (Rel. 34, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
HYPOTHETICAL 33.9 KD PROTEIN RV1996.
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317 אי
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PHYPOTHETICAL 18.6 KD PROTEIN IN TRPR-GPMB INTERGENIC REGION (F173).
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    Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Bacteria; Proteok
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DAC TO ACC
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N_SEQUENCE 1.0
YKFF_ECOLI
P75677;
15-JUL-1998 (
15-JUL-1998 (
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YURB_YEAST STANDARD; PRT; 196 AA.

P46989;

01-FEB-1996 (Rel. 33, Created)

01-FEB-1996 (Rel. 33, Last sequence update)

15-DEC-1998 (Rel. 37, Last annotation update)

HYPOTHETICAL 21.6 KD PROTEIN IN ATP12-RPL17B

YJL178C OR J0490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
OBERMALER B., PIRAVANDI E., RINKE M., DOMDEY H.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L26582; AAC36893.1; -. Hypothetical protein.
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Nucleic Acids Res. 22:1821-1829(1994).
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MEDLINE: 94268903.
ARVIDSON D.N., ARVIDSON C.G., LAWSON C.L., MINER J., ADAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
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TRANSMEM
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Protein; Transmembrane.
125 145 POTENTIAL.
196 AA; 21605 MW; AEA06F63 CRC32;
                                                                                 STANDARD;
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36, Created)
36, Last sequence
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MEDLINE; 92114051.

ODA K., YAMATO K., OHTA E., NAKAMURA Y., TAKEMURA M., NOZATO N.,

AKASHI K., KANEGAE T., OGURA Y., KOHCHI T., OHYAMA K.;

"Gene organization deduced from the complete sequence of liverwort

Marchantia polymorpha mitochondrial DNA. A primitive form of plant

mitochondrial genome.";

J. MOL. Biol. 223:1-7(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994
01-OCT-1994
01-OCT-1994
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PIR; S25969; S25969.
MENDEL; 2099; MARPO; ymf27;1.
Mitochondrion; Hypothetical
SEQUENCE 69 AA; 7940 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Strep
Marchantiales; Marchantiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marchantia polymorpha (Liverwort) Mitochondrion.
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SEQUENCE 79 AA;
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STRAIN-K12 / M01655;
MEDLINE; 97426617
BLATTINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEM G.F.,
GREEGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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HYPOTHETICAL
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AL 7.9 KD PROTEIN:
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                                                                                                                AAC09407.1; -.
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ROTEIN IN NAD6-NAD3 INTERGENIC
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ceae; Marchantia.
         protein.
699EE385 CRC32;
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YM27_MARPO

Length:

69

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14,

2000 08:03

Type:

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Check:

7679

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J., BURTON J., CONNELL.M., COPSEY T., COOPER J., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER

COULSON

SEQUENCE OF 53-170 FROM STRAIN-BRISTOL N2; MEDLINE; 94150718

N.A. the

Submitted (FEB-1994) to

EMBL/GenBank/DDBJ

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THE COLOR OF THE TRANSPORT OF THE FEET OF THE TRANSPORT O
! ! AA_SEQUENCE
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EMBL; X92494; CAA6173.1; ...
Hypothetical protein; Transmembrane.
Hypothetical protein; Transmembrane.
Byonain 25 33 POLY-SER.
DOMAIN 25 59 POTENTIAL.
TRANSMEM 35 57 77 POTENTIAL.
TRANSMEM 57 77 POTENTIAL.
172 24. 115510 MW; 11A8B5FA CRC32;
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01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
101-OCT-1996 (Rel. 3
1701266W OR N0800.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 19.1 KD PROTEIN PAR2.1 IN CHROMOSOME
KO2D10.5 OR PAR2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
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MEDLINE; 96310631.

SEN-GUPTA M., LYCK R., FLEIG U., NIEDENTHAL R.K., HEGEMANN J.H.;

"The sequence of a 24,152 bp segment from the left arm of chromosome strong saccharomyces cerevisiae between the BNI1 and the POL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNO6_YEAS
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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KD PROTEIN IN PIK1-POL2 INT
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Didea; Rhabditidae; Peloderinae; Caenorhabditis
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YNA1_CAEEL Length: 170 February 14, 2000 08:03
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nature 368:32-38(1994).
-!- SIMILARITY: TO PLASMID RK2 P116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LATRETILE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CLLAGHAN M., PARSONS J., PERCY C., RIFKEN L., RODPRA A., SAUNDERS D., SHOWNKEEN SIMS M., SANALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R., SULSTON J., THEERRY-MIEG J., THOMAS K., VAUDIM M., VAUGHAN K., WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDWAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      WILSON R., AINSCOUGH R., ANDERSON K., BAXNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPERT J., COOPER C.,
CRAXTON M., DEAR S., DU Z., DURBLIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KRESHAW J., KIRSTEN J., LAISSTER N.,
LATREILLE P., LIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
SIMS M., SMALDON N., SMITH A., SMITH M., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY MIEG. J., THOMAS K., VAUDIN M., VAUGHAN K.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WATERSON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J.,
WOLLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U00025; AAA50616.1; --
EMBL; L14710; AAA28082.1; ALT_INIT.
                                                                              Nature 368:32-38(1994).
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"2.2 Mb o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL
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WORMPEP; PAR2.1; CE
PFAM; PF00436; SSB;
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L-FEB-1994
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                                                                                                                Mb of contiguous nucleotide sequence from
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1 37.5
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28, Last sequence u.
29, Last annotation
KD PROTEIN R05D3.9
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institute. ...
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IN CHROMOSOME
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                                                                                                                          chromosome
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YNU6_CAEEL

Length: 381 protein. E 381 AA;

February 14, 2000 08:03 Type: P

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42878 MW;

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CRC32;

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LITPAMTLTR

AKIDMTIPRK

RKGFTSQHEK DLERLNLALD SIDFDPGAQE EEAEDMWHIY

GLEKFYEAVS

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PAQAADVAAV LHLKGRNIEE NLIRIGDIIK

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KETTEQRAKE

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51

VHTMLTVSVE DGTGFVVLMA

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01-FEB-1996 (Rel. 3
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01-NOV-1997 (Rel. 3
HYPOTHETICAL 42.9 K
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2; GARDINER A.;
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                                                      EMBL; 236238; CAA85277,1; -.
WORMPEP; R74.6; CE01059.
PFAM; PFOLOS; RF1; 1.
Hypothetical protein; Cell division; Meiosis; Mitosis
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33, Created)
33, Last sequence update)
35, Last annotation update)
KD PROTEIN R74.6 IN CHROMOSOME III.
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HALKEVLETP RANQELAIET

QVALRLADTK LLVADSLFRA

QDIETRRKYV

RLVESVREQN

AQGEVKALNQ FLELMSTEPD

RAFYGFNHVN

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I!AA_SEQUENCE 1.0

TO YOTC_CAEEL
AC 010120;

DT 01-FEB-1996 (F
DT 01-F
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                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD D., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DUTBIN R., FAVELLO A., FRASER A.,
FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISSTER N.,
LAITREILLE P., LIGHTNING J., LICYD C., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SIMS M., SMALDON N., SMITH A., SONNHAMMER E., STADEN R.,
SULSTON J., THIERRY MIEG J., THOMAS K., VAUDIN N., VAUGHAN K.,
WATISON R., WATSON A., WEINSTOCK L., WILKINSON-CDDOX--
"2.2 Mb of CONTINUAL."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                010120;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
01-FEB-1996 (Rel. 33, Last annotation
01-FEB-1996 (Rel. 36, Cast annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Phahditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14855; CAA32992.1; -. Hypothetical protein. SEQUENCE 232 AA; 26862 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 26.8 KD PROTEIN.
Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
Viruses; dsDNA viruses, no RNA stage; Lipothrixviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YORL_TTV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351
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on update)
13 IN CHROMOSOME
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I!AA_SEQUENCE 1.0
ID YOXD_BACSU
AC P14802;
DT 01-DEC-1992 (F
DT 01-DEC-1992 (F
DT 15-JUL-1998 (F
DT 15-JUL-1998 (F
DT 15-JUL-1998 (F
DE HYPOTHETICAL (F
DE HYPOTHETIC
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EMBL; 299114; CAB13743.1; ...
PIR; S01270; S01270.
HSSP; P1992; 2HSD.
SUBTILIST; B611048; YOXD.
PROM; PE00106; adh_Short; 1.
PFAM; PF00106; adh_Short; 1.
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AHN K.S., WAKE R.G.;
"Variations and coding for replication terminus of I gene 98:107-112(1991).
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a copyre the swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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01-DEC-1992 (Rel. 24, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN RTP-PELB INTERGENIC (ORF238)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 15:8501-8509(1987).
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CARRIGAN C.M., HAARSM.
"Sequence features of
subtilis chromosome."
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STRAIN=168;
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Bacteria; Firmicutes;
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4 NAD OR NADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   features of the sequence spanning the
f Bacillus subtilis 168 and w23 chromosomes.";
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                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 974.2617.
MEDLINE; 974.2617.
MEDLINE; F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., GOEDEN M.A., ROSE D.J.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Construction of a contiguous 874-kb sequence of the Escherichia contiguous 874-kb sequence of the Escherichia contiguous expension of the Linkage map and analysis of its sequence features."

DNA Res. 4:91-113(1997).

-I- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN DDG-GLK INTERGENIC REGION
                                                                                                                                  EMBL; AE000326; AAC75441.1; -. EMBL; D90868; CAB22182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97349980.

YAMAMOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K., YAMAMOTO Y., AIBA H., BABA T., MAKINO K., MIKI T., MITSUHASHI N., ITOH T., KUURA S., KITAGAWA M., MAKAMURA Y., NASHIMOTO H., MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H., SAITO N., SAMPEI G., SATOH Y., SIYASUNDARAM S., TAKAHASHI H., TAKEDA J., TAKEMOTO K., UEHARA K., WADA C., YAMAGATA S., HORIUCHI T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
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STRAIN-K12 / MG1655;
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                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12.";
science 277:1453-1474(1997).
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Length: 285
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238 AA;
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32355 MW;
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25299 MW;
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   February 14,
                                                      Transcription regulation; DNA-binding 9 H-T-H MOTIF (BY SIMILARITY). 2355 MW; 61FFAA84 CRC32;
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; 06381861 CRC32;
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THE PROPERTY OF SERVICE AND SE
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DYQQ_KLEPN STANDARD; PRT; 271 AA.

AC P27509;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE HYPOTHETICAL PROTEIN IN PQQA 5'REGION (ORF X)
DATE DESCOORS
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EMBL; L47709; AAB38444.1; -.
EMBL; Z99115; CAB14163.1; -.
SUBTILLST; BG11212; YPJG.
Hypothetical protein.
SEQUENCE 224 AA; 24806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-DEC-1998 (Rel.
HYPOTHETICAL 24.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-168 / MARBURG;
MEDLINE; 96349105
SOROKIN A.V., AZEVEDO V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPUG OR JOJG.
Bactllus subtilis.
Bactllus subtilis.
Bactllus/Clostridium group;
Bactllus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
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                                                               Klebsiella pneumoniae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERROR P.;
                                              Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENCE 1.0
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                                                                                                                                                                                                                                                                                                                                                                        INGFHQPDFV
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32, Last sequence update)
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                                                                     gamma subdivision; Enterobacteriaceae;
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SEQUENCE FROM N.A

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YPQQ_KLEPN Length: 271
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P77031; P76634; P76635;
01-NOV-1997 (Rel. 35, Cree
01-NOV-1997 (Rel. 35, Last
01-NOV-1997 (Rel. 35, Last
01-NOV-1997 (Rel. 35, Last
HYPOTHETICAL 46.8 KD PROTE
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STRAIN-K12 / MG1655;
MEDLINE: 97426617.
MAU B., SHAO Y.;
MAU B., SHAO Y.;
MAU B., SHAO Y.;
MAU B., SHAO Y.;
MEDLINE: 9742617.

                                              SEQUENCE FROM N.A.

STRAIN-K12;
AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
AIBA H., BABA T., ISONO K., ISONO S., ITOH T., KANAI K.,
KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M.,
KASHIMOTO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H.,
KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H.,
MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
SALTIO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C.,
YAMAMOTO Y., YANO M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1.0
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MOL. Gen. Genet. 232:284-294(1992).
-i- FUNCTION: NOT KNOWN.
-i- SIMILARITY: BELONGS TO PEPTIDAS!
-i- SIMILARITY: TO AN ORF IN THE 3'!
A.CALCOACETICUS.
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MEDLINE; 92212293.
MEULENBERG J.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria;
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PROSITE; PS
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      Submitted -! - SUBCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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   nitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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PS00869; F
                            (FEB-1997)
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35, Last sequence update)
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KD PROTEIN IN CYSJ-ENO INTERGENIC
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EMBL; AE000361; AAC75817.1;
DR EMBL; D90893; CAB22504.1;
DR ECOGENE; EGJ3174; YQCE.
ECOGENE; EGJ3174; YQCE.
TRANSHEM 49 69 POTENTIAL
VSMEM 49 97 117 POTENTIAL
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
MEDLINE; 97. PLUNKETT G
BLAITMER F.R., PLUNKETT G
REIGER J., DAVIS N.W., KI
                                                                                                                                                                                GREGOR J., L...
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01-NOV-1997
15-JUL-1998
15-JUL-1998
                                                                                                         Science
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 16.3 KD PROTEIN IN KDUI-LYSS INTERGENIC
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SEQUENCE OF 14-141 FROM N.A. STRAIN-K12 / MG1655;
ROBERTS D., ALLEN E., ARAUJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coll.
Racteria; Proteobacteria;
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                                                                                                                               complete genome sequence of 
nce 277:1453-1474(1997).
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                                                                                                                                                                                                                             T G. III, BLOCH C.I
S J., GLASNER F.D.
KIRKPATRICK H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPIIGHWQDT
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POTENTIAL.
886A1E5D CRC32;
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                                                                                                                                                                 Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                             C.A., PERNA N.T., BURLAND V.D., RODE C.K., MAYHEW G.F., A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPAAEAYRNM WLMGMAALGM
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I!AA_SEQUENCE 1.0
ID YRBC_HAEIN
AC P45028;
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                                                                  151 AMASAVDTVT
                                                                                                                                                                                                                                    EMBL; M55249; AAA23393.1; -.
PIR; JQ0857; JQ0857.
Transposable element; Hypothetical protein.
SEQUENCE 169 AA; 18129 MW; 9D36865A CRC32;
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Retron for the 67-base multicopy single-stranded DNA from Escherichia coli: a potential transposable element encoding reverse transcriptase and Dam methylase functions ", proc. Natl. Acad. Sci. U.S.A. 87:9454-9458(1990).
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LEW H., LIN D., NAMATH A., OEFNER P., SCHRAMM S., DAVIS
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
101-MAY-1991 (Rel. 18, Last annotation update)
HYPOTHETICAL 18,1 KD PROTEIN (ORFB) (RETRON EC67).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000369; AAC75888.1; ALT_INIT.
EMBL; U83187; AAB40288.1; -.
ECOGENE; EG13274; yqeK.
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STRAIN-CL-1;
MEDLINE; 91067724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia.
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P21316;
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                                                                                                                                     LTAPEIWLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INOUYE M.,
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              STANDARD
                                                                GLGASFGLL
                                                                                                                                   DLTEDSTLVD GFLAQIHCLP CVPINEVAKE KLPHYVMSAT
                                                                                                                                                                     HFDEACRAFA LRHNLVQLAE RAGMNVQILR NKLNPSQPHL
                                                                                                   VSGDVKTSAG
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                                                                                                   RRDAISSINS
              PRT;
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              214
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R.W.;
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IIAA_SEQUENCE 1.0
ID YRKG_BACSU
AC P54434;
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DT 01-0CT-1996 (F
DE HYPOTHETICAL 4
GN YRKG.
Bacillus subti
OC Bacteria; Firm
OC Bacillus/Stapl
RP SEQUENCE FROM
RC STRAIN-168 / (RA STRAIN-168 / (
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                                                                                       SEQUENCE FROM N.A.
STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M., N
SATO T., TAKEUCHI M.;
Submitted (MAY-1996) to th
                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
01-0CT-1996 (Rel. 34, Last annotation
HYPOTHETICAL 4.2 KD PROTEIN IN BLTR-SI
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STRAIN-ED / KW20:

MEDLINE; 95350630.

ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

FLEISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,

MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D.,

SCOTT J.D., SHRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDLOM E., COTTON M.D.,

WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDLOM E., COTTON M.D.,

TIME L.D., FRITCHHAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,

GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
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01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria: Firmicutes; Bacillus/Clostridium group:
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Signal. SIGNAL 1 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32788; AAC22740.1; -. TIGR; HI1084; -.
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL
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214 AA;
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(Rel. 32, Last sequence update)
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PROTEIN HI1084 PRECURSOR.
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; 24510 MW;
                                                                                              the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       MASUDA S., TAKEMARU K., HOSONO
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HYPOTHETICAL PROTEIN HI1084.
; 02256BEA CRC32;
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93642;

01-FEB-1995 (Rel. 3

01-FEB-1995 (Rel. 3

01-FEB-1995 (Rel. 3

01-FEB-1995 (Rel. 3

01-FEB-1946 (Rel. 3

01-FE
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
17-DEC-1999 (Rel. 39, Last annotation update)
18-DEC-1999 (Rel. 39, Last annotation update)
18-DEC-1999 (Rel. 39, Last annotation update)
18-DEC-1999 (Rel. 36, Last sequence update)
18-DEC-1999 (Rel. 36, Last sequence update)
18-DEC-1999 (Rel. 36, Last sequence update)
18-DEC-1998 (Rel. 36, Last sequence update)
18-DEC-1999 (Rel.
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GCOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRI: GCOLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRI: GCOLE S.T., BROSCH R., GAS S., BARRY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., DAVIER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J., CHURCHER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON TAYLOR K., WHITEHEAD S., BARRELL B.G.;

"Decliphering the biology of Mycobacterium tuberculosis from the complete genome sequence.",

"Decliphering the biology of Mycobacterium tuberculosis from the complete genome sequence.",

"Decliphering the biology of Mycobacterium tuberculosis from the complete genome sequence.",
                                                                                                                                                                                                                                                                                                                                                         101
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31. Last sequence update)
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KD PROTEIN IN ROCC-PTA INTERGENIC
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Bacillus subtilis

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!! AA_SEQUENCE
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                            15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
HYPOTHETICAL 31.6 F
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SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                     HYPOTHETICAL
F59C6.8.
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EMBL; Z99123; CAB15797.1; -.
PIR; S39739; S39739.
SUBTILIST; EG10630; YWFF.
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GLASER P., KUNST F., ARNAUD M., COUDART M.P., GONZALES W.,
HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., MOSZER I.
PRESECAN E., SANYANA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,
RAPOPORT G., DANCHIN A.;
"Bactillus subtilis genome project: cloning and sequencing of th
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
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TRANSMEM
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36, Last sequence update)
36, Last annotation updat
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YYVP_CAEEL
EMBL; L14063; AAA18532.1; -. MAIZEDB; 63528; -. PFAM; PF00891; Methyltransf_;
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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STRAIN-CV NKH31; TISSUE-ROOT;
STRAIN-CV NKH31; TISSUE-ROOT;
MEDLINE; 94105316.
JOHN I., WURTELE E.S., COLBERT J.T.;
HELD B.M., WANG H., JOHN I., WURTELE E.S., COLBERT J.T.;
HELD B.M., WANG H., JOHN I., WURTELE E.S., COLBERT J.T.;
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ZRP4_MAIZE
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO A FAMILY OF C.ELEGANS PROTEINS THAT GROUPS
C27A7_2, C33H5.2, C35A5.5, F13G3.3, F59C6.8, F49C12.5, R07B7.12
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyllophytes; Spermatophyta; Magnoliophyta; Lillopsida; Poales;
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Ol-FEB-1996 (Rel. 33, Last sequence update)
Ol-CCT-1996 (Rel. 34, Last annotation update)
OLETHYLIRANSFERASE ZRP4 (EC 2.1.1.-) (OMT).
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SIMILARITY: TO OTHER OMTS REQUIRING S-ADENOSYL-L-METHIONINE AS
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274 AA;
Methyltransf_2; 1.
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ZRP4_MAIZE Length: 364 February 14, 2000 08:03 Type: P
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                                                                                                                                   101
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                                                                                                  CIFKHTHGRG
 MVVGAGPSDM
                                DMFESIPPAD
                                                                 ISSLVDVGGG
                                                                                                                                 YTLTPVSRLL
                                                                                                                                                                AASLSQILSK VHLHPSRVSS LRRLMRVLTT INVFGTQPLG
                                                                                                                                                                                                MELSPNNSTD
                                AVLLKSVLHD WDHDDCVKIL KNCKKAIPPR EAGGKVIIIN
                                                                                                                                                                                                QSLLDAQLEL WHTTFAFMKS MALKSAIHLR IADAIHLHGG
                                                                                                IWELTKODAT FDALVNDGLA SDSQLIVDVA IKQSAEVFQG
                                                                                                                                 IGSQSSQLAQ
                                                                 IGAAAQAISK AFPHVKCSVL
 VY IMF INGME
                                                                                                                                 TPLAAMVLDP
                                                                                                                                                                                                                                                                  3067DB07 CRC32;
RDEQEWSKIF
                                                                                                                                 TIVSPFSELG
                                                                 DLAHVVAKAP
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